

1 31
TCG ACT ATG AAT GCT GAT ACT GCT CCA ACA TCT CCT TGT CCT TCC ATA TCT TCC CAG AAC
ser thr met asn ala asp thr ala pro thr ser pro cys pro ser ile ser ser gln asn

61 91
TCA AGC TCC TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC AGC ATG TTC GAT CGG ACT TCC
ser ser ser cys ser ser phe gln asp gln lys ile ala ser met phe asp arg thr ser

121 151 Cadherin
|xx EC motif xx|
AGA GTA CCC GCC AGC AGC ACT TCC TCA CCG GGG CTC CTC TTC ACA GAA CTG GCT GCT GCC
arg val pro ala ser ser thr ser ser pro gly leu leu phe thr glu leu ala ala ala

181 211
CTG GAT GCC GAA GGG GAA GGA ATC AGC GAA GTA CAA AGG AAA GCT GTC AGT GCA ATT CAC
leu asp ala glu gly glu gly ile ser glu val gln arg lys ala val ser ala ile his

241 271
AGC CTG CTA AGT TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA CCA GAG GTG AAG GTC AAA
ser leu leu ser ser his asp leu asp pro arg cys val lys pro glu val lys val lys

301 331
ATC GCC GCC CTT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT GCT TTG CCA CAG CTC TGT
ile ala ala leu tyr leu pro leu val gly ile ile leu asp ala leu pro gln leu cys

361 391
GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC TCG GAT GAA GAA CAA GAA
asp phe thr val ala asp thr arg arg tyr arg thr ser gly ser asp glu glu gln glu

421 451
GGA GCC GGT GCC ATT ACC CAG AAT GTG GCT CTG GCC ATA GCA GGG AAT AAT TTC AAT TTG
gly ala gly ala ile thr gln asn val ala leu ala ile ala gly asn asn phe asn leu

481 511
AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG TAC AAC ATG CTG AAC GCG
lys thr ser gly ile val leu ser ser leu pro tyr lys gln tyr asn met leu asn ala

541 571
GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG AAA AAT GCT GAT CAG AGC
asp thr thr arg asn leu met ile cys phe leu trp ile met lys asn ala asp gln ser

601 631
CTC ATT AGG AAG TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC AAC AGG ATT TTA GAT CTA
leu ile arg lys trp ile ala asp leu pro ser thr gln leu asn arg ile leu asp leu

661

CTT TTC ATC TGT GTG TTA TGT TTT GAG TAT AAG GGA AAA CAG AGT TCT GAC AAA GTC AGT
leu phe ile cys val leu cys phe glu tyr lys gly lys gln ser ser asp lys val ser

721

ACC CAA GTC CTG CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG GAA GAG GCT TTG CTG CGT
thr gln val leu gln lys ser arg asp val lys ala arg leu glu glu ala leu leu arg

781

GGG GAA GGG GCC AGA GGG GAG ATG ATG CGC CGC CGG GCT CCA GGG AAC GAC CGA TTT CCA
gly glu gly ala arg gly glu met met arg arg arg ala pro gly asn asp arg phe pro

841

GGC CTA AAT GAA AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT TGG CGG CAA GCT AAT GAG
gly leu asn glu asn leu arg trp lys lys glu gln thr his trp arg gln ala asn glu

901

AAG CTA GAT AAA ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG ATC AGT GGC AAT CTG GCT
lys leu asp lys thr lys ala glu leu asp gln glu ala leu ile ser gly asn leu ala

961

ACA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT ATC CAG GCG AGC TCG GCT
thr glu ala his leu ile ile leu asp met gln glu asn ile ile gln ala ser ser ala

1021

CTG GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG CTG GTG AAT TCT CTG AAC
leu asp cys lys asp ser leu leu gly gly val leu arg val leu val asn ser leu asn

1081

TGT GAT CAG AGT ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA CTC CGT GCT CTC ATC GCC
cys asp gln ser thr thr tyr leu thr his cys phe ala thr leu arg ala leu ile ala

1141

AAG TTT GGA GAC TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT TTC GAC CTA TGT CAC CAA
lys phe gly asp leu leu phe glu glu glu val glu gln cys phe asp leu cys his gln

1201

GTC CTG CAC CAC TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC CAA GCC TGT GCC ACC CTT
val leu his his cys ser ser ser met asp val thr arg ser gln ala cys ala thr leu

1261

TAC CTC CTC ATG AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT GCA AGA GTA AAG ATG CAA
tyr leu leu met arg phe ser phe gly ala thr ser asn phe ala arg val lys met gln

1321

GTA ACC ATG TCC CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC TTT AAT GAA GAG CAC CTG
val thr met ser leu ala ser leu val gly arg ala pro asp phe asn glu glu his leu

691

751

811

871

931

991

1051

1111

1171

1231

1291

1351

1381

AGA AGA TCC TTG AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC ACA GCC ATG CAG ATG ACT
arg arg ser leu arg thr ile leu ala tyr ser glu glu asp thr ala met gln met thr

1441

CCT TTT CCC ACC CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT AGC ATC TTA TAT GAC ACA
pro phe pro thr gln val glu glu leu leu cys asn leu asn ser ile leu tyr asp thr

1501

GTG AAA ATG AGG GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG GAT CTC ATG TAC AGA ATT
val lys met arg glu phe gln glu asp pro glu met leu met asp leu met tyr arg ile

1561

GCC AAG AGT TAC CAG GCA TCT CCT GAT CTG CGG CTG ACC TGG CTC CAG AAC ATG GCA GAG
ala lys ser tyr gln ala ser pro asp leu arg leu thr trp leu gln asn met ala glu

1621

AAA CAC ACC AAG AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC CTG GTG CAC GCC GCT GCG
lys his thr lys lys lys cys tyr thr glu ala ala met cys leu val his ala ala ala

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TTA GTG GCT GAG TAT CTG AGC ATG CTG GAG GAC CAC AGC TAC CTG CCC GTG GGC AGT GTC
leu val ala glu tyr leu ser met leu glu asp his ser tyr leu pro val gly ser val

1741

AGC TTC CAG AAT ATT TCT TCC AAT GTG CTG GAG GAG TCT GTG GTC TCT GAG GAC ACC CTG
ser phe gln asn ile ser ser asn val leu glu glu ser val val ser glu asp thr leu

1801

TCA CCT GAC GAG GAT GGG GTG TGC GCA GGC CAG TAC TTC ACC GAG AGT GGC CTG GTA GGC
ser pro asp glu asp gly val cys ala gly gln tyr phe thr glu ser gly leu val gly

1861

CTC CTG GAG CAG GCC GCG GAG CTC TTC AGC ACG GGA GGC TTA TAT GAG ACA GTT AAT GAG
leu leu glu gln ala ala glu leu phe ser thr gly gly leu tyr glu thr val asn glu

1921

GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA TTC CGG AAG CTG ACA CTC
val tyr lys leu val ile pro ile leu glu ala his arg glu phe arg lys leu thr leu

1981

ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC AAG GAT CAT AAG AGA ATG
thr his ser lys leu gln arg ala phe asp ser ile val asn lys asp his lys arg met

2041

TTT GGA ACC TAC TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT GGG GAT TTG GAT GAA CAG
phe gly thr tyr phe arg val gly phe phe gly ser lys phe gly asp leu asp glu gln

1411

1471

1531

1591

1711

1771

1831

1891

1951

2011

2071

2101

GAG TTT GTC TAC AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG ATC TCA CAT AGA CTA GAG
glu phe val tyr lys glu pro ala ile thr lys leu pro glu ile ser his arg leu glu

2131

2161

GCA TTT TAT GGT CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG ATT AAA GAC TCC ACT CCT
ala phe tyr gly gln cys phe gly ala glu phe val glu val ile lys asp ser thr pro

2191

2221

GTG GAC AAA ACC AAG TTG GAT CCT AAC AAG GCC TAC ATA CAG ATC ACT TTT GTG GAG CCC
val asp lys thr lys leu asp pro asn lys ala tyr ile gln ile thr phe val glu pro

2251

2281

TAC TTT GAT GAG TAT GAG ATG AAA GAC AGG GTC ACA TAC TTT GAG AAG AAT TTC AAC CTC
tyr phe asp glu tyr glu met lys asp arg val thr tyr phe glu lys asn phe asn leu

2311

2341

CGG AGG TTC ATG TAC ACC ACC CCG TTC ACC CTG GAG GGG CGG CCT CGG GGA GAG CTG CAT
arg arg phe met tyr thr thr pro phe thr leu glu gly arg pro arg gly glu leu his

2371

2401

GAG CAG TAC AGA AGG AAC ACA GTC CTG ACC ACT ATG CAC GCC TTC CCC TAC ATC AAG ACC
glu gln tyr arg arg asn thr val leu thr thr met his ala phe pro tyr ile lys thr

2431

2461

AGG ATC AGC GTC ATC CAG AAG GAG GAG TTT GTT TTG ACA CCG ATT GAA GTT GCC ATT GAA
arg ile ser val ile gln lys glu glu phe val leu thr pro ile glu val ala ile glu

2491

|xxxxxxxxxxxxxxxxxxxxxxxxxxxx

xx Coiled coil 1 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
GAC ATG AAG AAG AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC CAG GAG CCG CCT GAT GCA
asp met lys lys lys thr leu gln leu ala val ala ile asn gln glu pro pro asp ala

xx|

2611

AAG ATG CTI CAG ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT GTA AAT CAG GGA CCA CTG
lys met leu gln met val leu gln gly ser val gly ala thr val asn gln gly pro leu

2641

2671

GAA GTA GCC CAA GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA AAA CTC TAT CGA CAT CAC
glu val ala gln val phe leu ala glu ile pro ala asp pro lys leu tyr arg his his

2701

2731

|xxxxxxxxxxxx

AAC AAG TTG AGG TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT GGT GAA GCT GTA GAG AAA
asn lys leu arg leu cys phe lys glu phe ile met arg cys gly glu ala val glu lys

xx Coiled coil 2 xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
AAC AAG CGT CTC ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG GAA CTC AAA AAG AAC TAT
asn lys arg leu ile thr ala asp gln arg glu tyr gln gln glu leu lys lys asn tyr

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AAC	AAG	CTA	AAA	GAG	AAC	CTC	AGG	CCA	ATG	ATC	GAG	CGG	AAA	ATT	CCA	GAA	CTG	TAC	AAG
asn	lys	leu	lys	glu	asn	leu	arg	pro	met	ile	glu	arg	lys	ile	pro	glu	leu	tyr	lys

CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC AGA TCT AGT TTC AGG AAA
pro ile phe arg val glu ser gln lys arg asp ser phe his arg ser ser phe arg lys

TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA GAA AAG CCA TCT TCA TTC GTG GAG ACT GTG
cys glu thr gln leu ser gln gly ser OCH glu lys pro ser ser phe val glu thr val

GCC CTG CAA CCC TGG AGA AGG ACT TGC TGG TAC TTA AAA AAT GGG ACA TTT GCC ACC CAG
ala leu gln pro trp arg arg thr cys trp tyr leu lys asn gly thr phe ala thr gln

GAC TGA CTG TAC ACT CCC TGA TCA GCC AGC ACT CTG GAA GCT TTG GGA TCC CAG GAA CCA
 asp STP

TGG AAT TAT TCC CAA ATG GAC TCT GAC CAG ATT TTT GCC ATA CTG GGG GGT GGC GGG ATG

GAG GAT GGG TAC TCA GGC ATG ACT GCG TAT TTA TTA AAG TGT GTT TTT CCA CAA TGT ACC

3241
AAA CAA GGC ATA AGC AGC TTC TCC TGC TGA CTG GCC AAT CAC TGC CCA TCT GAG AGA TGA

TTT CCT CTG GCC CAT ATT TGA ATT TAT TGG AGT AAC TCA AAT TGC CTG AGG AAA AAT GGA

3361
AAA ATT ATC CAC CAG TCG ATT CAA ACT GAA TTT CAC TCT TTA TAG GAA GGC AGG GCA AAC

TTG TAG GAG TAC GAA ACA TTT TCA ATA AAT CTA CAA AGG GAA GCC TTA CTA CAA TTC CAA

3481
AAA TCA TCA TGG TTG GAA ATT TGG GAG GAG ATT ATT TGT GAA CTT GTT ACC CTT TTG GTA

ATG GIG GAC TAA TTG CTG TAT AGT TAT TTT TGT TTT ATT ATT ACT GTT ACA TTA ATT TAA

CAT GCA TTT ATA GAA GAA TAC ATT CAA AGC ACT GAT GTA GGA GAT ACA CGG TAC TTG GAG

3661

3721

CTT TGC TTT TTT TCT TAT GTC ACT CTT GTG TAC TAT CTA TTT TTC TCC TCT CTG GGA CCA

3751

3781

AGT TTC TTT TTA TAA AGC AAT AAT ATC TCT GTT TTC ATT TCA GAA CAT TGT GCT GTC TGT

3811

3841

CAG CAT ATG TAT ATC AGC TAC AAA ATA TAT TCA ACT TTG ACT TCT TTT GAC AAA GGA CTT

3871

3901

TAG GAA AAG GAG GAA CAA AGA CAT TAT TTG AGA ATT AAA TTA TAT ATT TTT AAT ATG ACT

3931

3961

GTG ACC TTG ACT GAT AAT AAA GAT GTA ATA AGA ATT GCA AGC TAA AAA AAA AAA AAA AAA

3991

4021

AAC TCG

.5 kb —

BRAIN
HEART
SKEL. MUSCLE
COLON
THYMUS
SPLEEN
KIDNEY
LIVER
SM..INTESTIN
PLACENTA
LUNG
PBL

Jurkat
MV4-11
THP
HL60
9D10
CH27
3A9
293

~ 7.5 kb —



B

HC2A
K1AA ASGNLDKNARFSAIYRQDSNKLSNDDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat
HC4
HC1
HC3
HC5

HC2A
K1AA FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
rat
HC4
HC1
HC3
HC5

HC2A
K1AA -----VLHHHQNPETYDEIK
rat KSFARKNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTSAFAAVLHHHQNPETYDEIK
HC4
HC1
HC3
HC5

HC2A
K1AA IELPTQLHEKHHLTLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPPLKDGRRVTSEQHI
rat IELPTQLHEKHHLTLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPPLKDGRRVTSEQHI
HC4
HC1
HC3
HC5

HC2A
K1AA PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
rat PVSANLPSGYLGYQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFFQYC
HC4
HC1
HC3 -----GPGPARSTVSISLISNSARV
HC5

HC2A
K1AA OKTESGAQALGNELVKYLKSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat OKTESGAQALGNELVKYLKSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEVAVNVTRV
HC4 -----MEIQVLI RFLSVILMQLFWVLPNMIHEDDVPISCPMV
HC1 -----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3 NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSNPSPSAES
HC5

HC2A I I H V V A Q C H E E G L S H L R S Y V K Y A K A E P Y V A S E Y K T V H E E L T K S T I L K P S A D F L T S N
 KIAA I I H V V A Q C H E E G L S H L R S Y V K Y A K A E P Y V A S E Y K T V H E E L T K S T I L K P S A D F L T S N
 rat -----
 HC4 L F H I V S K C H E E G L D S Y L S S F I K Y S F R P G K P S A P Q A P L I H E T L A T M M I A L L K Q S A D F L A I N
 HC1 L P D I V A K C H E E Q L D H S V Q S Y I K F V F K T R --- A C K E R P V H E D L A K N V T G L L K - S N D S P T V K
 HC3 T Q A M D R S C N R M S S H T E T S S F L Q T L T G R L P --- T K K L F H E E L A L Q W V V C S G --- S V R --- E
 HC5 -----

Cadherin
 Cleavage

HC2A K L L R Y S W F F F D V L I K S M A Q H L I E N S K V K L I R N Q F P A S Y H H A A E T V V N M L M P H I T Q K F G D
 KIAA K L L K Y S W F F F D V L I K S M A Q H L I E N S K V K L I R N Q F P A S Y H H A V E T V V N M L M P H I T Q K F R D
 rat -----
 HC4 K L L K Y S W F F F E I I A K S M A T Y L L E E N K I K L T H G Q R F P K A Y H H A L H S L F L A I T - I V E S Q Y A E
 HC1 H V L K H S W F F F A I I L K S M A Q H L I D T N K I Q L E R P Q R F P E S Y Q N E L D N L M V L S D H V I W K Y K D
 HC3 S A L Q Q A W F F F E L M V K S M V H H L Y F N D K L E A P R K S R F P E R F M D D I A A L V S T I A S D I V S R F Q K
 HC5 -----

HC2A N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S --- C F A P G D P K T L F E Y K F E F L
 KIAA N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S --- C F A P G D P K T L F E Y K F E F L
 rat -----
 HC4 I P K E S R N V N Y S L A S F L K C C L T L M D R G F V F N L I N --- D Y I S --- G F S P K D P K V L A E Y K F E F L
 HC1 A L E E T R R A T H S V A R F L K R C F T F M D R G C V F K M V N --- N Y I S --- M F S S G D L K T L C Q Y K F D F L
 HC3 E T E M V E R L N T S L A F F L N D L L S V M D R G F V F S L I K S C Y K Q V S S K L Y S L P N P S V L V S L R L D F L
 HC5 -----

HC2A F V V C N H E H Y I P L N L P M --- P F G K G R I Q R --- Y Q D L Q L --- D Y S L T D E F
 KIAA R V V C N H E H Y I P L N L P M --- P F G K G R I Q R --- Y Q D L Q L --- D Y S L T D E F
 rat -----
 HC4 Q T I C N H E H Y I P L N L P M --- A F A K P K L Q R --- V Q D S N L --- E Y S L S D E Y
 HC1 Q E V C Q H E H F I P L C L P I R S A N I P D L T P S E S --- T Q E L H A S D M P E Y S V T N E F
 HC3 F I I C S H E H Y V T L N L P C S L L T P A S P S P S V S S A T S Q S S G F S T N V Q D Q K I A N M F E L S --- V P F
 HC5 ----- M N A L T A P T S P C P S I S --- S Q N S S S C S S F Q D Q K I A S M F D R T S R V P A

Cadherin
 EC motif

HC2A C R N H F L V G L L L R E V G T A L Q E F R E --- V F L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T
 KIAA C R N H F L V G L L L R E V G T A L Q E F R E --- V F L I A I S V L K N L L I K H S F D D R Y A S R S H Q A R I A T
 rat -----
 HC4 C K H H F L V G L L L R E T S I A L Q D N Y E --- I R Y T A I S V I K N L L I K H A F D T R Y Q H K N Q Q A K I A Q
 HC1 C R K H F L I G I L L R E V G F A L Q E D O D --- V R H L A L A V L K N L M A K H S F D D R Y R E P R K Q A Q I A S
 HC3 F Q Q H Y L A G I V L T E L A V I L D P D A E G L F G L H K K V I N M V H N L L S S H D S D P R Y S D P Q I K A R V A M
 HC5 S S T S - S P G I L F T E L A A A L D A E G E G I S E V Q R K A V S A I H S L L S S H D L D P R C V K P E V K V K I A A

HC2A L Y L P L F G L L I E N V Q R I N V F D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H
 KIAA L Y L P L F G L L I E N V Q R I N V R D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H
 rat -----
 HC4 L Y L P F V G L L L E N I Q R L A G F D T L Y S C A A M P N S A S R D E F P C G --- F T S P --- A N --- R G S L S
 HC1 L Y M P L Y G M L L D N M P R I Y L K D L Y P F T V N T S N Q G S R D D L S T N G G F Q S Q T A I K H A N S V D T S F S
 HC3 L Y L P L I G I I M E T V P Q L Y D F T E T H N Q R G R P I C I A T D D Y E S E --- S G --- S M I S
 HC5 L Y L P L V G I I L D A L P Q L C D F T V A D T R R Y R --- T S G S D E E Q E --- G A --- G A I T

HC2A KDLLGAISCSPPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS
 KIAA KDLLGAISCSPPYTTSTPNINSVRNADSRGSLISTDSGNSLPERNSEKSNSLDKHQSS
 rat -----
 HC4 TDKDTAYGSGFQNG-----HGIKREDSRGS LIP-EGATGFPDQNGTGEN-----TRQS
 HC1 KDVLNSIAAFSS-----IAISTVNHADSRASLASLDSNPSTNEKSSSEKTDNCEKIPRPL
 HC3 QTVAMAIAGTSVPQ-----LTRPGSFLLTSTSGRQHT-----
 HC5 QNVALAIAGNNFN-----LKTSG-IVLSSLPYKQYN-----

HC2A TLGNSVVRCDKLDQSEIKSLLMCFLYILKMSDDALFTYWN-KASTSELMDDFFTISEVCL
 KIAA TLGNSVVRCDKLDQSEIKSLLMCFLYILKMSDDALFTYWN-KASTSELMDDFFTISEVCL
 rat -----
 HC4 STRSSVSQYNRLDQYEIRSLLMCYLYIVKMISEDTLITYWN-KVSPQELINILILEVCL
 HC1 ALIGSTLRFDRDQAETRSLLMCFHIMKTISETLIAYWQ-RAPSEVSDFFSILDVCL
 HC3 -----TFAESSRSLICLLWVLKN-ADETVLQKWFTDLSVLQNLRLDLLYLCLV
 HC5 -----MLNADTTBNLMICFLWIMKN-ADQSLIRKWIADLPSTQLNRILDLLFICV

HC2A HQFQYMGKRYIARNQEGLG--PIVHDRKS-----QTLPVSRNRTGMM
 KIAA HQFQYMGKRYIAR-----TGM
 rat -----
 HC4 FHFYMGKRNRIARVHDAWLSKHFGIDRKS-----QTMPALRNRSVGM
 HC1 QNFRYLGRNRIIRKIAAAF--KFVQSTQNNGLTKGSNPSCQTSGLLAQWMHSTSRHEGK
 HC3 SCFEYKGKGVFERMNSLTFFK--KSKDMRAK-----LEEAILGSGIARQEMV
 HC5 LCFEYKGKQSSDKVSTQVLQ--KSRDVKAR-----LEEALLRGEARGEMV

HC2A HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
 KIAA HARLQQL-----GSLDNS-----LTFNHSYGHSDADVLHQSLLEANIATEVC
 rat -----
 HC4 QARLQHL-----SSLESS-----FTLNHSSTTTEADIHFQALLEGNTATEVS
 HC1 QHRSQTLPIIRGK---NALSNPKL---LQMLDNTMTSNSNEIDIVHHVDTEANIATEGC
 HC3 RRSRGQLERSPSGSAFGSQENLRWKDMTHWRQNTKLDKSRAEIEHEALIDGNLATEAN
 HC5 RRRAPGNDRFP----GLNENLRWKKEQTHWRQANEKLDKTKAELDQEALISGNLATEAH

HC2A LTALDTLSLFTLAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRS LIY
 KIAA LTALDTLSLFTLAFKNQLLADHGHNPMLKKVFDVYLCFLQKHQSETALKNVFTALRS LIY
 rat -----KLSRGHSPMLKKVFDVYLCFLQKHQSEMAKNVFTALRS LIY
 HC4 LTVLDTISFFTQCFKTHFLNNDGHNPLMKKVFDIHLAFLKNGQSEVSLKHVFASLRAFIS
 HC1 LTILDVLSLFTQTHQRQLQQCDQNSLMKRGFDTYMLFFQVQNSATALKHVFASLRLFVC
 HC3 LIILDLTLEIVVQTVS--VTES--KESILGGVLKVLHSMACNSAVYLQHC FATQRALVS
 HC5 LIILDMQENIIQASS--ALDC--KDSLLGGVLRVLVNSLNCDSQSTTYLTHCFATLRALIA

HC2A KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH
 KIAA KFPSTFYEGRADMCAALCYEILKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH
 rat KFPSTFYEGRADMCASLCYEVLKCCNSKLSSIRTEASQLLYFLMRNNFDYTGKKS FVRTH
 HC4 KFPSAFFKGRVNMCAAFCEYVLKCCCTSKISSRNEASALLYLIMRNNFEYTKRKT FLRTH
 HC1 KFPSAFFQGPADLCGSFCYEVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKS IVRSH
 HC3 KFPPELLFEEETEQCADLCRLRLRHCS SIGTIRSHPSASLYLLMRQNF EIGN--N FARVK
 HC5 KFGDLLFEEVEQC FDLCHQVLHHCSSSMDVTRSQCACATLYLLMRFSFGATS--N FARVK

HC2A LQV IISVSQLIADVVGIGETR FQQSLSI INNCANS DR LIKHTSFSSDVKDLTKRIRTVLM
 KIAA LQV IISVSQLIADVVGIGETR FQQSLSI INNCANS DR LIKHTSFSSDVKDLTKRIRTVLM
 rat LQV IISLSQLIADVVGIGETR FQQSLSI INNCANS DR LIKHTSFSSDVKDLTKRIRTVLM
 HC4 LQIIIAVSQLIADVALSGSRFQESLFI INNFANS DR PMLARAFPAEVKDLTKRIRTVLM
 HC1 LQIIKAVSQLIAD-AGIGGSRFQHSIAITNNEFANGDKOMKNSNFP AEVKDLTKRIRTVLM

Transmembrane

HC2A	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGLSEAAAMCYVHV
KIAA	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGLSEAAAMCYVHV
rat	ATAQMKEHENDPEMLVDLQYSLAKSYASTPELRKRWLDSMARIHVKNGLSEAAAMCYVHV
HC4	ATAQMKEHEKDPEMLIDLQYSLAKSYASTPELRKRWLDSMAKIHARNGDLSEAAAMCYVHV
HC1	ATAQMKEHEKDPEMLVDLQYSLANSYASTPELRRTWLESMAKIHARNGDLSEAAAMCYIHI
HC3	DTVKMKEHQEDPEMLIDLMYRIAKGYQTS PDLRLTWLQNMAGKHSERSNHAEAAQCLVHS
HC5	DTVKMREFQEDPEMLMDLMYRIAKSYQAS PDLRLTWLQNMAEKHTKKKCYTEAAMCLVHA

	domain	SH3	
HC2A	TALVAEYITRKGV-----		-----FRQGCTAFRVITPN
KIAA	TALVAEYITRKEA-----	-----VQWEPPLPHSHSACLRRSRGGVFRQGCTAFRVITPN	
rat	TALVAEYITRKEAD-----	-----LALQREPPVPFYSHTSCQRKSRGGMFRQGCTAFRVITPN	
HC4	AALVAEFLHRKKL-----		-----FPNGCSAFKKITPN
HC1	AALIAEYIKRKGYWKVEKICTASLLSEDPHPCDSNSLLTTPSGGSFMFMGWPAFLSITPN		
HC3	AALVAEYLSMLED-----		-----RKYLPVGCVTFNISSN
HC5	AALVAEYLSMLED-----		-----HSYLPVGSVSFNISSN

ITAM

HC2A	IDEEASMMEDVGMQD-----VHFNEVDVLMELLEQCADGLWKAERYELIADIYKLIPI
KIAA	IDEEASMMEDVGMQD-----VHFNEVDVLMELLEQCADGLWKAERYELIADIYKLIPI
rat	IDEEASMMEDVGMQD-----VHFNEVDVLMELLEQCADGLWKAERLRAGLLTSINSSSP
HC4	IDEEGAMKEDAGMMD-----VHYSEEVLLLELLEQCVNGLWKAERYELISEISKLIGPI
HC1	IKEEGAAKEDSGMHD-----TPYENILVEQLYMCGEFLWKSEYELIADVNKPIIAV
HC3	VLEESAVSDDVSPDEEGICSGKYFTESGLVGLLEQAAASFMSAGMYEAVNEVYKVLPIPI
HC5	VLEESVVSSEDTLSPDEDGVCAGQYFTESGLVGLLEQAAELFSTGGLYETVNEVYKVLPIPI

	ITAM	ITAM	ITAM	ITAM
HC2A	YEKRRD-----			
KIAA	YEKRRDFEPLAHLIDTTHRAYSKYTEVMHSGRRLGTYFRVAFFGQAAQYQTDSETDVE			
rat	SMKSGGTLETTHLYDTTHRRYSKYTEVITR-----A-----AGSWDLLPGGLFGQ			
HC4	YENRFEFENLTQVYRTIHGAYTKILEVMHTKKRLLG-----TFFRVAFYFGQ			
HC1	FEKQDFKFLSDLYDYDHRSYLKVAEVVNSEKRLFG-----HYFRVAFYFGQ			
HC3	HEANFDAKFLSTIHGKLQEAFSKIVHQSTGWERMFG-----TYFRVGFYFG-			
HC5	LEAHPEFRFLTLTHSKLQRAFDSIVNKDH--KRMFG-----TYFRVGFFG-			

	ITAM	ITAM
HC2A	-FFEDEDGKEYIYKEPKLTPLEISIQRLKLYSDRFGSENVKMIQDSGKVNPKDLDSKYA	
KIAA	GFFEDEDGKEYIYKEPKLTPLEISIQRLKLYSDRFGSENVKMIQDSGKVNPKDLDSKYA	
rat	GFFEDEDGKEYIYKEPKLTPLEISIQRLKLYSDRFGSENVKMIQDSGKVNPKDLDSKYA	
HC4	SFFEEDDGKEYIYKEPKLTGLSEISLRLVKLYGEKFGTENVKIIQDSKVNAKELDPKYA	
HC1	GFFEEEEGKEYIYKEPKLTGLSEISIQRLKLYADKFGADNVKIIQDSKNVNPKDLDPKYA	
HC3	TKFGDLDEQEFVYKEPAITKLAEISHPLEGFGYGERFGEDVVEVIKDSNPVDCKLDPNKA	
HC5	SKFGDLDEQEFVYKEPAITKLPEISHPLEAFYGOFGAEFVEVIKDSNPVDKTKLDPNKA	

ITAM

HC2A	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKROGGVEEQCKRRTILTA
KIAA	YIQVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKROGGVEEQCKRRTILTA
rat	YIQVTHVTPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKROGGVEEQCKRRTILTA
HC4	HIQVTVYKPYFDDKELTERKTEFERNHNI SRFVFEAPYTLGSKKQGCIEEQCKRRTILTT
HC1	YIQVTVYVTPFFEEKEIEDRKTD FEMHHNINRFVFETPFTLSGKKHGGVAEQCKRRTILTT

Coiled-Coil 1

HC2A	IHC	F	P	V	V	K	K	R	I	P	V	M	Y	Q	H	H	T	D	L	N	F	I	E	V	A	I	D	E	M	S	K	K	V	A	E	L	R	Q	L	C	S	S	A	E	V	D	M	I	K	L	Q	L	K	L	Q	S	V		
KIAA	I	H	C	F	P	V	V	K	K	R	I	P	V	M	Y	Q	H	H	T	D	L	N	F	I	E	V	A	I	D	E	M	S	K	K	V	A	E	L	R	Q	L	C	S	S	A	E	V	D	M	I	K	L	Q	L	K	L	Q	S	V
rat	I	H	C	F	P	V	V	K	K	R	I	P	V	M	Y	Q	H	H	T	D	L	N	F	I	E	V	A	I	D	E	M	S	K	K	V	A	E	L	H	Q	L	C	S	S	A	E	V	D	M	I	K	L	Q	L	K	L	Q	S	V
HC4	S	N	S	F	P	V	V	K	K	R	I	P	I	N	C	E	Q	Q	I	N	L	K	F	I	D	G	A	T	D	E	I	K	D	K	T	A	E	L	Q	K	L	C	S	S	T	D	V	D	M	I	Q	L	Q	L	K	L	Q	S	V
HC1	S	H	L	F	P	V	V	K	K	R	I	Q	V	I	S	S	S	T	E	L	N	F	I	E	V	A	I	D	E	M	S	R	K	V	S	E	L	N	Q	L	C	T	M	E	E	V	D	M	I	S	L	Q	L	K	L	Q	S	V	
HC3	S	H	A	F	P	Y	I	K	T	R	V	N	V	T	H	K	E	E	I	I	L	T	F	I	E	V	A	I	D	M	Q	K	T	Q	E	L	A	F	A	T	H	Q	D	P	A	D	P	K	M	L	Q	M	V	L	Q	S	V		
HC5	M	H	A	F	P	Y	I	K	T	R	I	S	V	I	Q	K	E	E	F	V	L	T	F	I	E	V	A	I	D	M	K	K	T	L	Q	L	A	V	A	I	N	Q	E	P	P	D	A	K	M	L	Q	M	V	L	Q	S	V		

Coiled-Coil 2

HC2A	S	V	Q	V	N	A	G	P	L	A	Y	A	R	A	F	L	D	D	T	N	T	K	R	Y	P	D	N	K	V	K	L	L	K	E	V	F	R	Q	F	V	E	A	C	G	Q	A	L	A	V	N	E	R	L	I	K	E	D	Q	L	E
KIAA	S	V	Q	V	N	A	G	P	L	A	Y	A	R	A	F	L	D	D	T	N	T	K	R	Y	P	D	N	K	V	K	L	L	K	E	V	F	R	Q	F	V	E	A	C	G	Q	A	L	A	V	N	E	R	L	I	K	E	D	Q	L	E
rat	S	V	Q	V	N	A	G	P	L	A	Y	A	R	A	F	L	D	D	T	N	T	K	R	Y	P	D	N	K	V	K	L	L	K	E	V	F	R	Q	F	V	E	A	C	G	Q	A	L	A	V	N	E	R	L	I	K	E	D	Q	L	E
HC4	S	V	Q	V	N	A	G	P	L	A	Y	A	R	A	F	L	N	D	S	Q	A	S	K	Y	P	P	K	V	S	E	L	K	D	M	F	R	K	F	I	Q	A	C	S	I	A	L	E	L	N	E	R	L	I	K	E	D	Q	V	E	
HC1	S	V	K	V	N	A	G	P	M	A	Y	A	R	A	F	L	E	E	T	N	A	K	K	Y	P	D	N	Q	V	K	L	L	K	E	I	F	R	Q	F	A	D	A	C	G	Q	A	L	D	V	N	E	R	L	I	K	E	D	Q	L	E
HC3	G	T	T	V	N	Q	G	P	L	E	V	A	Q	V	L	S	E	I	P	S	D	F	K	L	F	R	H	H	N	K	L	R	L	C	F	K	D	F	T	K	R	C	E	D	A	L	R	K	N	K	S	L	I	G	P	V	Q	K		
HC5	G	A	T	V	N	Q	G	P	L	E	V	A	Q	V	L	S	E	I	P	A	D	F	K	L	Y	R	H	H	N	K	L	R	L	C	F	K	E	F	I	M	R	C	G	E	A	V	E	K	N	E	R	L	I	T	A	D	Q	R		

Coiled-Coil 2

HC2A	Y	Q	E	M	K	A	N	Y	F	E	M	A	K	E	L	S	E	I	M	H	E	Q	I	C	P	L	E	E	K	T	S	-	V	L	P	N	S	L	H	I	F	N	A	I	S	G	T	P	T	S	T	M	V	H	G	M	T	S
KIAA	Y	Q	E	M	K	A	N	Y	F	E	M	A	K	E	L	S	E	I	M	H	E	Q	L	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-							
rat	Y	Q	E	M	K	A	N	Y	F	E	I	R	K	E	L	S	D	I	I	V	E	R	I	C	P	G	E	D	K	R	A	T	K	F	P	A	H	L	Q	R	H	Q	R	D	T	N	K	H	S	G	S	R	V	D	Q	F	I	L
HC4	Y	H	E	G	L	K	S	N	F	R	D	M	V	K	E	L	S	D	I	I	H	E	Q	I	L	Q	E	D	T	M	H	S	P	W	M	S	N	T	L	H	V	F	C	A	I	S	G	T	S	S	D	R	G	Y	G	S	P	
HC1	Y	Q	E	L	R	S	H	Y	K	D	M	L	S	E	L	S	T	V	M	N	E	Q	I	T	G	R	D	D	L	S	K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-						
HC3	Y	Q	R	E	L	G	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-								
HC5	Y	Q	Q	E	L	K	K	N	Y	N	K	L	K	E	N	L	R	P	M	I	E	R	K	I	P	E	L	Y	K	P	I	F	R	V	E	S	Q	K	R	D	S	F	H	R	S	S	F	R	C	E	T	Q	L	S	Q			

PBM

HC2A	S	S	V	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				
KIAA	S	S	V	V	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				
rat	C	V	T	L	P	H	E	P	H	V	G	T	C	F	V	M	C	K	L	R	T	T	F	R	A	N	H	W	F	C	Q	A	Q	E	E	A	M	G	N	G	R	E	K	E	P	W	T	V	I	F	N	S	R	F
HC4	E	V	Z	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				
HC1	S	A	E	V	Z	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				
HC3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				
HC5	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-				

HC2A	-	-	-	-
KIAA	-	-	-	-
rat	V	H	I	F
HC4	-	-	-	-
HC1	-	-	-	-
HC3	-	-	-	-
HC5	-	-	-	-

CLASP-1
KIAA1058
CLASP-2
CLASP-6
CLASP-4
DOCK180
DOCK2
DOCK3
KIAA0716
CLASP-3
CONSENSUS

A	B
YRVAFYGO:::GFFEEEGKEYIYKEP	
FRVAFPGDAQYQFTDSETDVEGFFFEDEOGKEYIYKEP	
	FEDEOGKEYIYKEP
FRVAFPGO:::GFFFEDEOGKEYIYKEP	
FRVAFYGO:::SFFFEDEOGKEYIYKEP	
FVAGYYGO:::GFPTFLRGKVFIYRGKEYERRED	
FVAGYYGO:::GFPSFLRNKVFIYRGKEYERRED	
FRVGfyGR:::KFPFFLRNKEYVCRGH	
FRVGfyGK:::KFPFFLRNKEFVCRGH	
FRVGfyGT:::KFGDLDEQEFVYKEP	
F V FYG	KEY K
YF	Q F R

TRG
CLASP-1
CLASP-2
CLASP-4
CLASP-3
KIAA0716
DOCK3
DOCK2
DOCK180
CONSENSUS

C
PKLTPLSEISORLLKLYSDKFGSENVKMIQDSGKVNPKDLDKSKFAYIQVTHVTPFFDEKE
PKLTGLSEISORLLKLYADKFGADNVKIIQDSNKNVPKDLDPKYAYIQVTYVTPFFEEKE
PKLTPLSEISORLLKLYSDKFGSENVKMTQDSGKVNPKDLDKSKYAYIQVTHVIPFFDEKE
PKLTGLSEISLRVLKLYGEKFGTENVKIIQDSDKVNAKELDPKYAYIQVTYVKPYFDQKE
PAITKLAEISHRLEGFYGERFGEDVVEVIKDSNPVDKCKLDPNKAYIQITYVEPYFDTYE
HDYERLEAFQQRMLNEFPFAIA-----MQHANQPDETIFQAEAOYLQIYAVTPIPEBQE
HDYERLEAFQQRMLSEFPQAVA-----MQHPNHPDDAILQCDAAQLQIYAVTPIPDYVD
FQMQLMTQFPNAEK-----MNTTSAPGDDVKNAPOGYIQCFVQPVLDDEHP
EYERREDFQMQLMTQFPNAEK-----MNTTSAPGDDVKNAPOGYIQCFVQPVLDDEHP
L L Y
M F
YIQ+ V P D
L E

D	E
RTILTTSHLFPYVKKRIQVISQSSTELNPIEVAIDEMSRKVSELN	
RTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELH	
RTILTAIHCFPYVKKRIPVMYQHHTDLNPIEVAIDEMSKKVAELR	
RTILTAIHCFPYVKKRIPVMYQHHTDLNPIEV:HDEMSSKKVAELR	
RTILTTNSFPYVKKRIPINCEQQINLKPIDVATDEIKDKTAELO	
RTILTTSHAFPIYIKTRVNVTHKEEIIILTPIEVAIEDMOKKTQELA	
NTVLTTMHAFPIYIKTRISVIQKEEFVLTPIEVAIEDMOKKTQLOLA	
FTSLYLVSPLPGISRWFVEVEKREVVEMSPLENAIEVLENKKNQOLK	
RTSEVVTAYKLPGILRWFEVVHMSQTTISPLENAIETMSTANEKIL	
RTTLTLTHSLPGISRWFEVERRELVEVSPLENAIQVVENKKNQELR	
RTSEVVTAYKLPGILRWFEVVHMSQTTISPLENAIETMSTANEKIL	
RT L FP V + V + P+E AI+ M +L	
F L L + I	

ref 1.1 ↓

1
TCG ACT ATG AAT GCT GAT ACT GCT CCA ACA TCT CCT TGT CCT TCC ATA TCT TCC CAG AAC
ser thr met asn ala asp thr ala pro thr ser pro cys pro ser ile ser ser gln asn

61
TCA AGC TCC TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC AGC ATG TTC GAT CGG ACT TCC
ser ser ser cys ser ser phe gln asp gln lys ile ala ser met phe asp arg thr ser

121
AGA GTA CCC GCC AGC AGC ACT TCC TCA CCG GGG CTC CTC TTC ACA GAA CTG GCT GCT GCC
arg val pro ala ser ser thr ser ser pro gly leu leu phe thr glu leu ala ala ala

181
CTG GAT GCC GAA GGG GAA GGA ATC AGC GAA GTA CAA AGG AAA GCT GTC AGT GCA ATT CAC
leu asp ala glu gly glu gly ile ser glu val gln arg lys ala val ser ala ile his

241
AGC CTG CTA AGT TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA CCA GAG GTG AAG GTC AAA
ser leu leu ser ser his asp leu asp pro arg cys val lys pro glu val lys val lys

301
ATC GCC GCC CTT TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT GCT TTG CCA CAG CTC TGT
ile ala ala leu tyr leu pro leu val gly ile ile leu asp ala leu pro gln leu cys

361
GAC TTT ACA GTT GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC TCG GAT GAA GAA CAA GAA
asp phe thr val ala asp thr arg arg tyr arg thr ser gly ser asp glu glu gln glu

421
GGA GCC GGT GCC ATT ACC CAG AAT GTG GCT CTG GCC ATA GCA GGG AAT AAT TTC AAT TTG
gly ala gly ala ile thr gln asn val ala leu ala ile ala gly asn asn phe asn leu

461
AAA ACA AGT GGA ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG TAC AAC ATG CTG AAC GCG
lys thr ser gly ile val leu ser ser leu pro tyr lys gln tyr asn met leu asn ala

541
GAC ACT ACT CGC AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG AAA AAT GCT GAT CAG AGC
asp thr thr arg asn leu met ile cys phe leu trp ile met lys asn ala asp gln ser

601
CTC ATT AGG AAG TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC AAC AGG ATT TTA GAT CTA
leu ile arg lys trp ile ala asp leu pro ser thr gln leu asn arg ile leu asp leu

661
CTT TTC ATC TGT GTG TTA TGT TTT GAG TAT AAG GGA AAA CAG AGT TCT GAC AAA GTC AGT
leu phe ile cys val leu cys phe glu tyr lys gly lys gln ser ser asp lys val ser

721
ACC CAA GTC CTG CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG GAA GAG GCT TTG CTG CGT
thr gln val leu gln lys ser arg asp val lys ala arg leu glu glu ala leu leu arg

841
GGC CTA AAT GAA AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT TGG CGG CAA GCT AAT GAG
gly leu asn glu asn leu arg trp lys lys glu gln thr his trp arg gln ala asn glu

901
AAG CTA GAT AAA ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG ATC AGT GGC AAT CTG GCT
lys leu asp lys thr lys ala glu leu asp gln glu ala leu ile ser gly asn leu ala

961
ACA GAA GCA CAT TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT ATC CAG GCG AGC TCG GCT
thr glu ala his leu ile ile leu asp met gln glu asn ile ile gln ala ser ser ala

1021
CTG GAC TGT AAA GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG CTG GTG AAT TCT CTG AAC
leu asp cys lys asp ser leu leu gly gly val leu arg val leu val asn ser leu asn
↓ ref 3.1

1081
TGT GAT CAG AGT ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA CTC CGT GCT CTC ATC GCC
cys asp gln ser thr thr tyr leu thr his cys phe ala thr leu arg ala leu ile ala

1141
AAG TTT GGA GAC TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT TTC GAC CTA TGT CAC CAA
lys phe gly asp leu leu phe glu glu glu val glu gln cys phe asp leu cys his gln

1201
GTC CTG CAC CAC TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC CAA GCC TGT GCC ACC CTT
val leu his his cys ser ser ser met asp val thr arg ser gln ala cys ala thr leu

1261
TAC CTC CTC ATG AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT GCA AGA GTA AAG ATG CAA
tyr leu leu met arg phe ser phe gly ala thr ser asn phe ala arg val lys met gln

1321
GTA ACC ATG TCC CTG GCA TCT TTG GTG GGA AGA GCA CCA GAC TTT AAT GAA GAG CAC CTG
val thr met ser leu ala ser leu val gly arg ala pro asp phe asn glu glu his leu

1381
AGA AGA TCC TTG AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC ACA GCC ATG CAG ATG ACT
arg arg ser leu arg thr ile leu ala tyr ser glu glu asp thr ala met gln met thr

1441
CCT TTT CCC ACC CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT AGC ATC TTA TAT GAC ACA
pro phe pro thr gln val glu glu leu leu cys asn leu asn ser ile leu tyr asp thr

1501
GTG AAA ATG AGG GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG GAT CTC ATG TAC AGA ATT
val lys met arg glu phe gln glu asp pro glu met leu met asp leu met tyr arg ile

1561
GCC AAG AGT TAC CAG GCA TCT CCT GAT CTG CGG CTG ACC TGG CTC CAG AAC ATG GCA GAG
ala lys ser tyr gln ala ser pro asp leu arg leu thr trp leu gln asn met ala glu

1621
AAA CAC ACC AAG AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC CTG GTG CAC GCC GCT GCG

1681	1711
TTA GTG GCT GAG TAT CTG AGC ATG CTG GAG	GAC CAC AGC TAC CTG CCC GTG GGC AGT GTC
leu val ala glu tyr leu ser met leu glu	asp his ser tyr leu pro val gly ser val
1741	1771
AGC TTC CAG AAT ATT TCT TCC AAT GTG CTG	GAG GAG TCT GTG GTC TCT GAG GAC ACC CTG
ser phe gln asn ile ser ser asn val leu	glu glu ser val val ser glu asp thr leu
1801	1831
TCA CCT GAC GAG GAT GGG GTG TGC GCA GGC	CAG TAC TTC ACC GAG AGT GGC CTG GTA GGC
ser pro asp glu asp gly val cys ala gly	gln tyr phe thr glu ser gly leu val gly
1861	1891
CTC CTG GAG CAG GCC GCG GAG CTC TTC AGC	ACG GGA GGC TTA TAT GAG ACA GTT AAT GAG
leu leu glu gln ala ala glu leu phe ser	thr gly gly leu tyr glu thr val asn glu
1921	1951
GTC TAC AAG CTG GTC ATC CCC ATC CTA GAA	GCG CAT CGA GAA TTC CGG AAG CTG ACA CTC
val tyr lys leu val ile pro ile leu glu	ala his arg glu phe arg lys leu thr leu
1981	2011
ACT CAC AGC AAG CTG CAG AGA GCC TTC GAC	AGC ATC GTT AAC AAG GAT CAT AAG AGA ATG
thr his ser lys leu gln arg ala phe asp	ser ile val asn lys asp his lys arg met
2041	2071
TTT GGA ACC TAC TTC CGA GTT GGT TTC TTT	GGA TCC AAA TTT GGG GAT TTG GAT GAA CAG
phe gly thr tyr phe arg val gly phe phe	gly ser lys phe gly asp leu asp glu gln
2101	2131
GAG TTT GTC TAC AAA GAG CCT GCA ATT ACC	AAG CTT CCT GAG ATC TCA CAT AGA CTA GAG
glu phe val tyr lys glu pro ala ile thr	lys leu pro glu ile ser his arg leu glu
2161	2191
GCA TTT TAT GGT CAA TGT TTT GGT GCA GAA	TTT GTG GAA GTG ATT AAA GAC TCC ACT CCT
ala phe tyr gly gln cys phe gly ala glu	phe val glu val ile lys asp ser thr pro
↓ ref 4.1	
2221	2251
GTG GAC AAA ACC AAG TTG GAT CCT AAC AAG	GCC TAC ATA CAG ATC ACT TTT GTG GAG CCC
val asp lys thr lys leu asp pro asn lys	ala tyr ile gln ile thr phe val glu pro
2281	2311
TAC TTT GAT GAG TAT GAG ATG AAA GAC AGG	GTC ACA TAC TTT GAG AAG AAT TTC AAC CTC
tyr phe asp glu tyr glu met lys asp arg	val thr tyr phe glu lys asn phe asn leu
2341	2371
CGG AGG TTC ATG TAC ACC ACC CCG TTC ACC	CTG GAG GGG CGG CCT CGG GGA GAG CTG CAT
arg arg phe met tyr thr thr pro phe thr	leu glu gly arg pro arg gly glu leu his
2401	2431
GAG CAG TAC AGA AGG AAC ACA GTC CTG ACC	ACT ATG CAC GCC TTC CCC TAC ATC AAG ACC
glu gln tyr arg arg asn thr val leu thr	thr met his ala phe pro tyr ile lys thr
2461	2491
AGG ATC AGC GTC ATC CAG AAG GAG GAG TTT	GTT TTG ACA CCG ATT GAA GTT GCC ATT GAA
arg ile ser val ile gln lys glu glu phe	val leu thr pro ile glu val ala ile glu

2521
 GAC ATG AAG AAG AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC CAG GAG CCG CCT GAT GCA
 asp met lys lys lys thr leu gln leu ala val ala ile asn gln glu pro pro asp ala

2551
 2611
 AAG ATG CTT CAG ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT GTA AAT CAG GGA CCA CTG
 lys met leu gln met val leu gln gly ser val gly ala thr val asn gln gly pro leu

2641
 GAA GTA GCC CAA GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA AAA CTC TAT CGA CAT CAC
 glu val ala gln val phe leu ala glu ile pro ala asp pro lys leu tyr arg his his

2671
 2731
 AAC AAG TTG AGG TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT GGT GAA GCT GTA GAG AAA
 asn lys leu arg leu cys phe lys glu phe ile met arg cys gly glu ala val glu lys

2761
 AAC AAG CGT CTC ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG GAA CTC AAA AAG AAC TAT
 asn lys arg leu ile thr ala asp gln arg glu tyr gln gln glu leu lys lys asn tyr

2791
 2851
 AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA ATT CCA GAA CTG TAC AAG
 asn lys leu lys glu asn leu arg pro met ile glu arg lys ile pro glu leu tyr lys

2881
 2911
 CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC AGA TCT AGT TTC AGG AAA
 pro ile phe arg val glu ser gln lys arg asp ser phe his arg ser ser phe arg lys

2941
 2971
 TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA GAA AAG CCA TCT TCA TTC GTG GAG ACT GTG
 cys glu thr gln leu ser gln gly ser OCH
 ref 5.1

3001
 3031
 GCC CTG CAA CCC TGG AGA AGG ACT TGC TGG TAC TTA AAA AAT GGG ACA TTT GCC ACC CAG

3061
 3091
 GAC TGA CTG TAC ACT CCC TGA TCA GCC AGC ACT CTG GAA GCT TTG GGA TCC CAG GAA CCA

3121
 3151
 TGG AAT TAT TCC CAA ATG GAC TCT GAC CAG ATT TTT GCC ATA CTG GGG GGT GGC GGG ATG

3181
 3211
 GAG GAT GGG TAC TCA GGC ATG ACT GCG TAT TTA TTA AAG TGT GTT TTT CCA CAA TGT ACC

3241
 3271
 AAA CAA GGC ATA AGC AGC TTC TCC TGC TGA CTG GCC AAT CAC TGC CCA TCT GAG AGA TGA

3301
 3331
 TTT CCT CTG GCC CAT ATT TGA ATT TAT TGG AGT AAC TCA AAT TGC CTG AGG AAA AAT GGA

3361
 3391
 AAA ATT ATC CAC CAG TCG ATT CAA ACT GAA TTT CAC TCT TTA TAG GAA GGC AGG GCA AAC

3421
 3451
 TTG TAG GAG TAC GAA ACA TTT TCA ATA AAT CTA CAA AGG GAA GCC TTA CTA CAA TTC CAA

AAA TCA TCA TGG TTG GAA ATT TGG GAG GAG ATT ATT TGT GAA CTT GTT ACC CTT TTG GTA
 3541 3571
 ATG GTG GAC TAA TTG CTG TAT AGT TAT TTT TGT TTT ATT ATT ACT GTT ACA TTA ATT TAA
 3601 3631
 CAT GCA TTT ATA GAA GAA TAC ATT CAA AGC ACT GAT GTA GGA GAT ACA CGG TAC TTG GAG
 3661 3691
 CAG TCA GCC AAA AAT CAC AGA TAC TGC TTT CAC TTA AAT GGA AAC AAT TCT CCG ATA ATG
 3721 3751
 CTT TGC TTT TTT TCT TAT GTC ACT CTT GTG TAC TAT CTA TTT TTC TCC TCT CTG GGA CCA
 3781 3811
 AGT TTC TTT TTA TAA AGC AAT AAT ATC TCT GTT TTC ATT TCA GAA CAT TGT GCT GTC TGT
 3841 3871
 CAG CAT ATG TAT ATC AGC TAC AAA ATA TAT TCA ACT TTG ACT TCT TTT GAC AAA GGA CTT
 3901 3931
 TAG GAA AAG GAG GAA CAA AGA CAT TAT TTG AGA ATT AAA TTA TAT ATT TTT AAT ATG ACT
 3961 3991
 GTG ACC TTG ACT GAT AAT AAA GAT GTA ATA AGA ATT GCA AGC TAA AAA AAA AAA AAA AAA
 4021
 AAC TCG

References

BAC sequences of Human CLASP 5

Ref 1.1

Sequence of BAC19 using primer HC5S11, which spans nucleotides 3-22 of the cDNA. Exon sequence is underlined and represents nucleotides 32-57.

CTCTCTGTCTTCATATCTTCCAGGTTATAAAGNATTATTTACTAAAAGAANATTCANGC
 TATTTTCATTTAACTAGCTCAGTTTAATCATGTATTTCTATAAAGGTTAGTCTTATTAAT
 TTGACAAAACAATCAAACAATTCAAACCAGATCAAGTATGCTACCCTGAAGTTACACC
 ACTAGCTAAGAATTAACAATCTAAGTAATTGGTTTTCTCCCCAGGCTCAAGGCTCCCTGA
 TCAGGTAAAGTAAAGCCAAGAATCCAATAAGCCCTATGAAATTTAGAACTCATAGAA
 AAGTCTCAAATCTTCTTGTCTGACATTAGCCAATTGTTATATTATGCAAATAGAGGATT
 NCAAGTAAATAAGTTTGGAACCTGTTTACCAGGTTTTTGCAGCAGNCCTCTAAGAGCTT
 AACTGGTCATGCATTGAATGCCGAGAGCAAAGAGGAATGGAGAGGGGNTGTAAGNGG
 TTCCAATNTTACTGGAACCCACCACTATCTTTNGAAGTCTTGATACTTAACTGNGTGTA
 GNCTCTTTAGGCCTNTANTAANTAGAATCTATATGGATTTCGTGTTCTGTCNGCAAGNAG
 TGCCTATGAAA

Ref 2.1

Sequence of BAC19 using primer HC5AS10b, which spans nucleotides 560-580 of the cDNA. Exon sequence is underlined and represents nucleotides 510-553.

TGCGAGTAGTGTCGCGTTCAGCATGTTGTACTGCTTATAGGGCTGAAGGGAGGCACG
ATTGGGGGATGGAGGCCAGGGAAGAAGTCAAGCAACAGAAAAATTTGAGGCTTAACA
GTCAAGCAACAGAAAAATTCAAAGTGTTCTCTTAAAATACCATGACTGTACATCACTG
CTAGGCTGGAGATCTATTGCCAGTAGCCCTGCCTTCCCTAGGCAGGGGAAGCTGTGTT
CTTTGAGTAGCGCTACTCAGCAAAGAGGCTCACCTGGGGCAGTATTTGAGCTAGGCTT
TCAGCCACCGTATCTGAGTACCTCTGTCTTANGAGCAGTGTGGCCTGGTGATCACCCCT
GGGCCTTGATCATGCGTGCTGCAATCCCAAGTGATACAAAGAGGCTTTCATGCTGCTAA
GATCTCCAAGTATTTCTCCTTCGTGCTGGGCAGCAGAGGGTTAGACTTNCAGGGGGAGA
AGGAAACTGGCTGGGTGCCATGAATAANCTTGCTGTTCAAGANTTAACCTTCTTTGTTAC
ATAAGNGCAAAGGTATAACATAAAGGGNCATGAACTGCTCAACNAAATTNATCAAAT
CCATGTTTGTGGGAGTTCTTTTGTNATNGGAAGTTTAACCCCTAA

Ref 3.1

Sequence of BAC13 using primer C5S3, which spans nucleotides 1086-1105 of the cDNA. Exon sequence is underlined and represents nucleotides 1110-1120.

CCNGCTCTTTTTGGCAANGTAANCTTGGGATGCTTGTTTTCTTCCTCTTAATTAAGAG
NAAGANTTTTTTAGCTTCATACTTCTCTCTTCAGGGGGACCAAAAGTCACAGAGCATA
TTAAGTGGCANAACCCCNAAAGGTCTTAAGTCTTCCTAGGAAGAAAGCAGATGCCCTGA
TTCTGTGGGAAGCCACCATGGAGAGGAAAAGCAGTGGCTCCCATATTTGAAGTGNGGA
CCTAACTCTAGAAAGTTTAAAANGGCCATTTGCTGAAGGGCTATGACATGAGAACAGA
GATCAACTGAGTGACTTAGCAANTTCACTCTTTCTCTGTAANACCTCTGGTGAGTGAGA
NTAAATCCTNTATGTGACGCCCATTAGTCTTACAAAANGTCATGCCNTAAAATGCCAN
GAAGGNCAGAAATGAATTTCTCACCGCCNGAGGAATGAGGATTATNCTGGGGGGACA
TGCANAAATATTNNNCCCCCNATTTATTNATTTATTTATTTTGGAGACNGAGTNTCGNT
CTAATCGCCCCCAGGCTGGNAGGTGGNAGGTGGTTCCCATCTTNAANCTTANNTNGGA
AGGNCCTCTTTGNGCCCCNGGGGGGNGNAAAGNGAATTCCTAAATGCCTNCANNCCC
CTCCCTGGANGTTATTTGGGGGNNTTNTAAAGGGCNGTGGCNG

Ref 4.1

Sequence of BAC13 using primer C5S7, which spans nucleotides 2196-2205 of the cDNA. . Exon sequence is underlined and represents nucleotides 2225-2231.

ACAAAACTAACCATCANTCTCTAAATCCCAACAANCTTTTTTTAAGAATACCTAANG
AGCTCAACNAGGGGGACTNTCCAANGCACTTAAATGCAGNCAAACNACNCCNNCAAG
AGNGGCAACTACTAATGGGGCANATCTNAAAGAAAATATAGNCAAAGGNNGGAATCA
TAATAGGAGCNAGCACTTANGAAGGACCAACTGGGGAGCCGCAACTGNATNAGCN

TTCCTANNNTAGAGANGAGANAACTGGGGACATGGGAAGAGGNAAGCGAAGGGTTCA
AGGGGANGNAAGCGAGCAGANNCCAGGGNCTCANACTNGNGGGGNNTGGGGGGNTN
CTGNNCCCTACNCTTNGNANGAACAGNGNNGTTGANNTGGCTTTNGANTA

Ref 5.1

Sequence of BAC13 using primer 122047F1, which spans nucleotides 3537-3556 of the cDNA.
Exon sequence is underlined and represents nucleotides 3000-3492. This region does not contain a
intron in this region

CCANNAGATTNTTGNAACGNNGGTAGGCTTCCTTTGTAGATTTATTGAAAATGTTTCGT
ACTTCTACAAGTTTGCCTGCCTTCCTATAAAGAGTGAAANTCANTTTGAATCGACTGG
TGGATAATTNTCCATTTTTCCTCAGGCAATTTNGAGTTACTCCAATAAAATCAAATAT
GGGCCAGAGGAAATCATCTTCAGATGGGCAGTGATTGGCCAGTCAGCAGGAGAAGC
TGCTTATGCCTTGTTTGGTACATTGTGGAAAAACACACTTTAATAAATACGCANTCATG
CCTGAGTACCCATCCTCCATCCCGCCACCCCCCAGTATGGCAAAAATCTGGTCAGAGT
CCATTTGGGAATAATTCCATGGTTCCTGGGATCCCAAAGCTTCCAGAAGTGCTGGCTG
ATCAANGGAGTGTACAGTCAGTCCTGGGTGGCAAAAATGTCCCATTTTTTAAGTACCA
AGCAAAGGTTCTTCTNCAAGGGTTNCTAGGGCC

Figure
Multiple sequence alignment of Human CLASP proteins with intron/exon borders indicated by a vertical line. Numbers in right margin correspond to References

HC2A	-----
KIAA	ASGNLDKNARFSAIYRQDSNKLSDMLKLLADFRKPEKMAKLPVILGNLDITIDNVSSD
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----
KIAA	FPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKHTQPYTIYTNHLYVYPKYLKYDSQ
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	-----VLHHHQNPETYDEIK
KIAA	KSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPVFTSAFAAVLHHHQNPETYDEIK
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	IELPTQLHEKHHLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
KIAA	IELPTQLHEKHHLTFFHVSCDNSSKGSTKKRDVVETQVGYSWLPLLKDGRVVTSEQHI
rat	-----
HC4	-----
HC1	-----
HC3	-----
HC5	-----
HC2A	PVSANLPSGYLGQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYC
KIAA	PVSANLPSGYLGQELGMGRHYGPEIKWVDGGKPLLKISTHLVSTVYTQDQHLHNFQYC
rat	-----
HC4	-----
HC1	-----
HC3	-----GPGPARSTVSIISLISNSARV
HC5	-----
HC2A	QKTESGAQALGNELVKYLKSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEVAVNVTRV
KIAA	QKTESGAQALGNELVKYLKSLHAMEGHVMI AFLPTILNQLFRVLT-RATQEEVAVNVTRV
rat	-----
HC4	-----MEIQVLIRFLSVILMQLFWVLPNMIHEDDVPI SCPMV
HC1	-----MSFLPIILNQLFKVLV-QNEEDEITTTVTRV
HC3	NRSRSLSNSNPDISGTPTSPDDEVRSIIGSKGLDRSNSWVNTGGPKAAPWGSPSPSAES
HC5	-----

HC2A I I H V V A Q Y G L E S H L R S Y V K Y A Y K A E P Y V A S E Y K T V H E E L T I L K P S A D F L T S N
 KIAA I I H V V A Q Y G L E S H L R S Y V K Y A Y K A E P Y V A S E Y K T V H E E L T I L K P S A D F L T S N
 rat -----
 HC4 L F H I V S K C H E E G L S Y L S S F I K Y S F R P G K P S A P Q A P L I H E T L A T M M I A L L K Q S A D F L A I N
 HC1 L P D I V A K C H E E Q L D H S V Q S Y I K F V F K T R --- A C K E R P V H E D L A K N V T G L L K - S N D S P T V K
 HC3 T Q A M D R S C N F M S S H T E T S S F L Q T L T G R L P --- T K K L F H E E L A L Q W V V C S G --- S V F --- E
 HC5 -----

Cadherin
 Cleavage

HC2A K L L R Y S W F F F D V L I K S M A Q H L I E N S K V K L I R N Q R F P A S Y H H A A E T V V N M L M P H I T Q K F G D
 KIAA K L L K Y S W F F F D V L I K S M A Q H L I E N S K V K L I R N Q R F P A S Y H H A V E T V V N M L M P H I T Q K F R D
 rat -----
 HC4 K L L K Y S W F F F E I I A K S M A T Y L L E E N K I K L T H G Q R F P K A Y H H A L H S L F L A I T - I V E S Q Y A E
 HC1 H V L K H S W F F F A I I L K S M A Q H L I D T N K I Q L E R P Q R F P E S Y Q N E L D N L V M V L S D H V I W K Y K D
 HC3 S A L Q Q A W F F F E L Y V K S M V H H L Y F N D K L E A P R K S R F P E R F M D D I A A L V S T I A S D I V S R F Q K
 HC5 -----

HC2A N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S --- C F A P G D P K T L F E Y K F E F L
 KIAA N P E A S K N A N H S L A V F I K R C F T F M D R G F V F K Q I N --- N Y I S --- C F A P G D P K T L F E Y K F E F L
 rat -----
 HC4 I P K E S R N V N Y S L A S F L K C C L T I M D R G F V F N L I N --- D Y I S --- G F S P K D P K V L A E Y K F E F L
 HC1 A L E E T R R A T H S V A R F L K R C F T F M D R G C V F K M V N --- N Y I S --- M F S S G D L K T L C Q Y K F D F L
 HC3 D T E M V E R L N T S L A F F L N D L L S V M D R G F V F S L I K S C Y K Q V S S K L Y S L P N P S V I V S L R L D F L
 HC5 -----

HC2A R V V C N H E H Y I P L N L P M --- P F G K G R I Q R --- Y Q D L Q L --- D Y S L T T E F
 KIAA R V V C N H E H Y I P L N L P M --- P F G K G R I Q R --- Y Q D L Q L --- D Y S L T T E F
 rat -----
 HC4 Q T I C N H E H Y I P L N L P M --- A F A K P K L Q R --- V Q D S N L --- E Y S L S L E Y
 HC1 Q E V C Q H E H F I P L C L P I R S A N I P D L T P S E S --- T Q E L H A S D M P E Y S V T N E F
 HC3 R I I C S H E H Y V T L N L F C S L L T P P A S P S P V S S A T S Q S S G F S T N V Q D Q K I A N M F E L S --- V P F
 HC5 --- M N A D T A P T S P C P S I S --- S Q S S S C S S F Q D Q K I A S M F D R T S R V P A

Cadherin
 EC motif

HC2A C R N H F L V G L L L R E V G T A L Q E F R E --- V R L I A I S V L K N L L I K H S F D R Y A S R S H Q A R I A T
 KIAA C R N H F L V G L L L R E V G T A L Q E F R E --- V R L I A I S V L K N L L I K H S F D R Y A S R S H Q A R I A T
 rat -----
 HC4 C K H H F L V G L L L R E T S I A L Q D N Y E --- I R Y T A I S V I K N L L I K H A F D T R Y Q H K N Q Q A K I A Q
 HC1 C R K H F L I G L L L R E V G F A L Q E D Q D --- V R H L A L A V L K N L M A K H S F D D R Y R E P R K Q A Q I A S
 HC3 R Q Q H Y L A G L V L T E L A V I L D P D A E G L F G L H K K V I N M V H N L L S S H D S D P R Y S D P Q I K A R V A M
 HC5 S S T S - S P G L L F T E L A A A L D A E G E G I S E V Q R K A V S A I H S L L S S H D L D P R C V K F E V K V K I A A

HC2A L Y L P L F G L L I E N V Q R I N V R D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H
 KIAA L Y L P L F G L L I E N V Q R I N V R D V S P F P V N A G - M T V K D E S L A L P A V N P L V T P Q K G S T L D N S L H
 rat -----
 HC4 L Y L P F V G L L E N I Q R L A G R D T L Y S C A M P N S A S R D E F P C G --- F T S P --- A N --- R G S L S
 HC1 L Y M P L Y G M L L D N M P R I Y L K D L Y P F T V N T S N G S R D D L S T N G G F Q S Q T A I K H A N S V D T S F S
 HC3 L Y L P L I G I M E T V P Q L Y D F T E T H N Q R G R P I C I A T D D Y E S E --- S G --- S M I S
 HC5 L Y L P L V G I I L D A L P Q L C D F T V A D T R R Y R --- T S G S D E E Q E --- G A --- Q R I T

2.1

2.1

2.1

2.1

3.1

3.1

3.1

Transmembrane

HC2A	ATAQMKHEHNDPEMLVDLQYSLAKSYASTPELRKKTWLD SMARIHVKNGLSEAAAMCYVHV
KIAA	ATAQMKHEHNDPEMLVDLQYSLAKSYASTPELRKKTWLD SMARIHVKNGLSEAAAMCYVHV
rat	ATAQMKHEHNDPEMLVDLQYSLAKSYASTPELRKKTWLD SMARIHVKNGLSEAAAMCYVHV
HC4	ATAQMKHEHNDPEMLVDLQYSLAKSYASTPELRKKTWLD SMARIHVKNGLSEAAAMCYVHV
HC1	ATAQMKHEHNDPEMLVDLQYSLAKSYASTPELRKKTWLD SMARIHVKNGLSEAAAMCYVHV
HC3	DTVKMKEHQEDPEMLIDLMYRIAGYQTSDDLRLTWLQNMAGKHSERSHAEAAQCLVHS
HC5	DTVKMKEHQEDPEMLIDLMYRIAKSYQASDDLRLTWLQNMAGKHTKKKCYTEAAMCLVHA

	domain	SH3	
HC2A	TALVAEYLTRKGV-----		FRQGCTAFRVITPN
KIAA	TALVAEYLTRKEA-----	VQWEPPLPHSHSACLRRSRGGVFRQGCTAFRVITPN	
rat	TALVAEYLTRKEAD-----	LALQREPPVPYPYSHTSCQRKSRGGMFRQGCTAFRVITPN	
HC4	AALVAEYLHKKKL-----		FPNGCSAFKKITPN
HC1	AALIAEYLKRGYKVEKICTASLLSEDPHPCDSNSLLTTPSGGSMFSGMWPAPFLSITPN		
HC3	AALVAEYLSMLEL-----		RKYLPGVCVTFQNISSN
HC5	AALVAEYLSMLEL-----		HSYLPVGSVSFQNISSN

ITAM

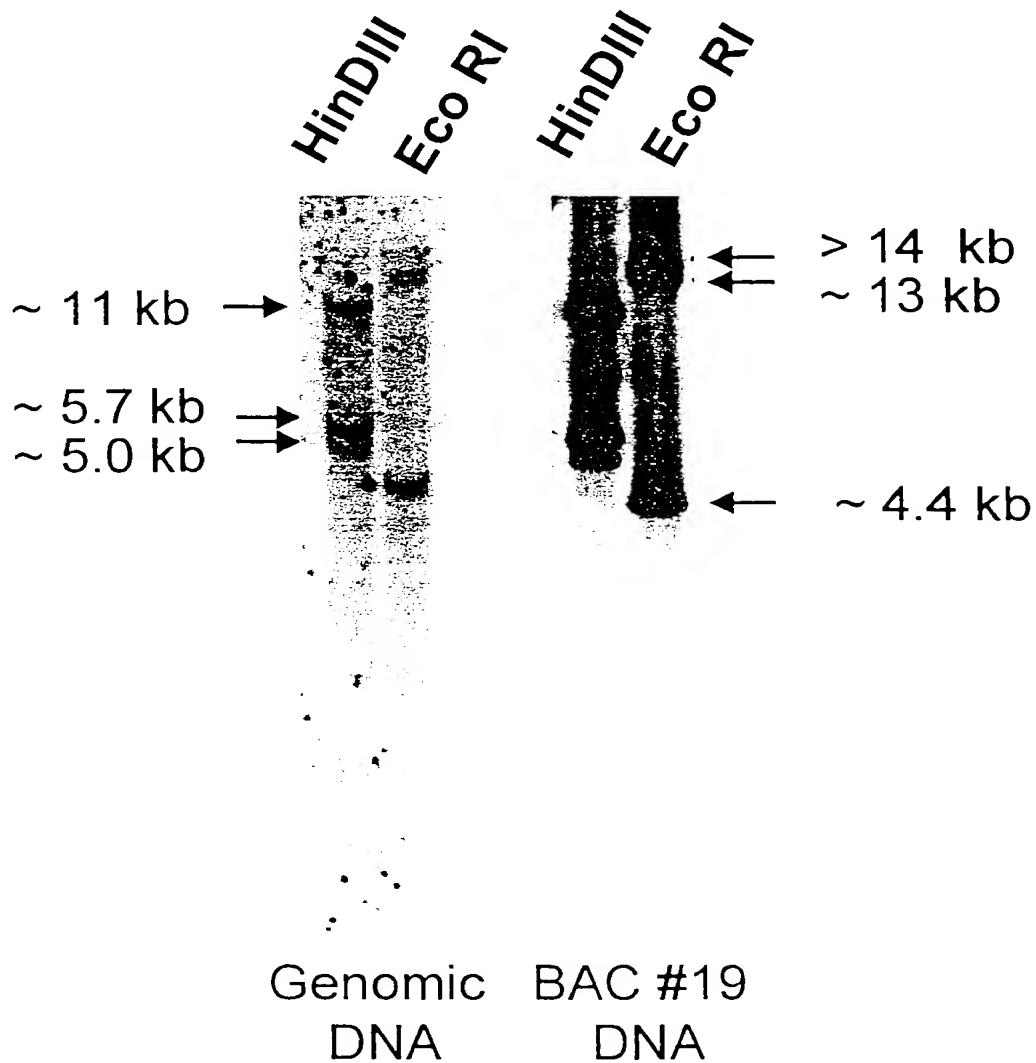
HC2A	IDEEASMMEDVGMQD-----	VHFNEVDVLMELLEQCADGLWKAER	YELIADIYKLIPI
KIAA	IDEEASMMEDVGMQD-----	VHFNEVDVLMELLEQCADGLWKAER	YELIADIYKLIPI
rat	IDEEASMMEDVGMQD-----	VHFNEVDVLMELLEQCADGLWKAERLRAGLLTSINSSSP	
HC4	IDEEGAMKEDAGMMD-----	VHYSEVLLLELLEQCVNGLWKAER	YELIADIYKLIPI
HC1	IKKEGAAKEDSGMHD-----	TPYNEINILVEQLYMCGEFLWKSEH	YELIADIYKLIPI
HC3	VLEESAVSDDDVSPDEEGICSGKYFTESGLVGLLEQAAASFMSMAGMYEAVNEVYKLIPI		
HC5	VLEESVVSSEDLTSPDEDDGVCAGQYFTESGLVGLLEQAALFTSGGLYETVNEVYKLIPI		

	ITAM	ITAM	ITAM	ITAM
HC2A	YEKRRD-----			
KIAA	YEKRRDFERLAHLYDTIHRAYSKVTEVMHSGRLLGT	TYFRVAFFGQAQYQFTDSETDVE		
rat	SMKSGGTLETTHLYDTIHRAYSKVTEVITR-----	A-----	AGSWDLLPGGLFGQ	
HC4	YENRREFENLTQVVRTIHGAYTKILEVMHTKKRLG-----			TFFRVAFYSG
HC1	FEKQDFKLLSDLYDDHRSYLYKVAEVVNSEKRLFG-----			TYFRVAFYSG
HC3	HEANRDAKLLSTIHGKLOEAFSKIIVHQTGWERMFG-----			TYFRVAFYSG
HC5	LEAHREFRKLTLTHSKLQRAFDSIVNKDH--KRMFG-----			TYFRVAFYSG

	ITAM	ITAM
HC2A	-FFEDEDGKEYIYKEPKLTPLSEISQRLKLYSDHFGSENVKMIQDSGKVNPKDLDSHYA	
KIAA	GFFEDEDGKEYIYKEPKLTPLSEISQRLKLYSDHFGSENVKMIQDSGKVNPKDLDSHYA	
rat	GFFEDEDGKEYIYKEPKLTPLSEISQRLKLYSDHFGSENVKMIQDSGKVNPKDLDSHYA	
HC4	SFFEEDGKEYIYKEPKLTGLSEISLRLVKLYGEGFTENVKIIQDSGKVNAKELDPHYA	
HC1	GFFEEDGKEYIYKEPKLTGLSEISQRLKLYADHFGADNVKIIQDSGKVNPKDLDPHYA	
HC3	TKFGDLDEQEFVYKEPAITKLAEISHRLAQYGERFGEDVVEVIKDSNPVDKCKLDPNKA	
HC5	SKFGDLDEQEFVYKEPAITKLPEISHRLAEYGGQFGAEFVEVIKDSNPVDKCKLDPNKA	

ITAM

HC2A	YIDVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
KIAA	YIDVTHVIPFFDEKELQERKTEFERSHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
rat	YIDVTHVIPFFDEKELQERKTEFERCHNIRRFMFEMPFTQTGKRQGGVEEQCKRRTILTA
HC4	HIQVTVYKPYFDDKELTERKTEFERHNINISRFVFEAPYTLGKKGQCCIEEQCKRRTILTT
HC1	YIQVTVYVTPFFEEKEIEDRKTDFFEMHHNINIRFVFETPTLSGKKHGGVAEQCKRRTILTT
HC3	YIQVTVYVTPFFDYEMKDRITYFDKNYNLRRFMCTPFTLDGRAHGEHQFCKRRTILTT



-111

CGGTAACCGCCATTTTGTCTCCTGTAACAATTTACGCGCGTGTAAGTCTTTCAAAGCCTCAGTTTTATGACC
CTGTGGAGCCAGTGSACTTTGAAGGACTTCTG -1

1/1	ATG	ACA	CAC	CTG	AAC	AGC	CTG	GAT	GTG	CAG	CTT	GCC	DAG	GAG	CTC	GGG	GAC	TTC	ACT	GAT
	Met	thr	his	leu	asn	ser	leu	asp	val	gln	leu	ala	gln	glu	leu	gly	asp	phe	thr	asp
61/21	GAC	GAC	TTG	GAC	GTG	GTG	TTC	ACG	CCA	AAG	GAA	TGT	AGG	ACT	TTG	CAG	CCC	TCT	TTG	CCG
	asp	asp	leu	asp	val	val	phe	thr	pro	lys	glu	cys	arg	thr	leu	gln	pro	ser	leu	pro
121/41	GAG	GAA	GGG	GTT	GAA	CTG	GAC	CCT	CAT	GTC	AGG	GAC	TGT	GTT	CAG	ACC	TAC	ATC	CGT	GAG
	glu	glu	gly	val	glu	leu	asp	pro	his	val	arg	asp	cys	val	gln	thr	tyr	ile	arg	glu
181/61	TGG	CTA	ATC	GTG	AAC	CGG	AAA	AAC	CAA	GGA	AGT	CCA	GAA	ATC	TGT	GGC	TTT	AAA	AAG	ACT
	trp	leu	ile	val	asn	arg	lys	asn	gln	gly	ser	pro	glu	ile	cys	gly	phe	lys	lys	thr
241/81	GGA	TCT	CGA	AAA	GAT	TTT	CAC	AAG	ACG	CTT	CCG	AAA	CAG	ACG	TTT	GAG	TCG	GAA	ACC	TTG
	gly	ser	arg	lys	asp	phe	his	lys	thr	leu	pro	lys	gln	thr	phe	glu	ser	glu	thr	leu
301/101	GAG	TGC	AGT	GAA	CCC	GCT	GCT	CAG	GCA	GGC	CCC	CGC	CAC	TTA	AAC	GTG	CTG	TGC	GAC	GTG
	glu	cys	ser	glu	pro	ala	ala	gln	ala	gly	pro	arg	his	leu	asn	val	leu	cys	asp	val
361/121	TCT	GGG	AAA	GGC	CCC	GTC	ACT	GCC	TGT	GAC	TTT	GAC	CTC	CGC	AGC	CTG	CAG	CCT	GAC	AAG
	ser	gly	lys	gly	pro	val	thr	ala	cys	asp	phe	asp	leu	arg	ser	leu	gln	pro	asp	lys
421/141	CGG	CTA	GAA	AAC	CTC	CTG	CAG	CAA	GTG	AGT	GCC	GAG	GAC	TTT	GAG	AAG	CAG	AAC	GAG	GAG
	arg	leu	glu	asn	leu	leu	gln	gln	val	ser	ala	glu	asp	phe	glu	lys	gln	asn	glu	glu
481/161	GCC	CGG	AGG	ACC	AAC	AGG	CAG	GCC	GAG	CTC	TTT	GCC	CTT	TAC	CCA	TCA	GTG	GAC	GAG	GAG
	ala	arg	arg	thr	asn	arg	gln	ala	glu	leu	phe	ala	leu	tyr	pro	ser	val	asp	glu	glu
541/181	GAT	GCT	GTG	GAA	ATA	CGT	CCA	GTA	CCA	GAA	TGT	CCC	AAG	GAA	CAC	CTG	GGC	AAC	AGA	ATA
	asp	ala	val	glu	ile	arg	pro	val	pro	glu	cys	pro	lys	glu	his	leu	gly	asn	arg	ile
601/201	TTG	GTC	AAG	TTG	CTG	ACC	TTG	AAG	TTC	GAG	ATT	GAA	ATT	GAG	CCC	CTG	TTT	GCC	AGC	ATT
	leu	val	lys	leu	leu	thr	leu	lys	phe	glu	ile	glu	ile	glu	pro	leu	phe	ala	ser	ile
661/221	GCC	CTC	TAC	GAT	GTT	AAA	GAA	AGG	AAA	AAG	ATC	TCA	GAA	AAT	TTT	CAC	TGT	GAC	CTG	AAC
	ala	leu	tyr	asp	val	lys	glu	arg	lys	lys	ile	ser	glu	asn	phe	his	cys	asp	leu	asn
721/241	TCT	GAC	CAG	TTT	AAA	GGA	TTT	CTG	CGA	GCT	CAC	ACG	CCT	TCA	GTG	GCC	GCA	TCA	AGT	CAG
	ser	asp	gln	phe	lys	gly	phe	leu	arg	ala	his	thr	pro	ser	val	ala	ala	ser	ser	gln
781/261	GCG	AGA	TCT	GCA	GTC	TTC	TCA	GTC	ACC	TAC	CCG	TCC	TCA	GAC	ATC	TAC	CTG	GTA	GTC	AAG
	ala	arg	ser	ala	val	phe	ser	val	thr	tyr	pro	ser	ser	asp	ile	tyr	leu	val	val	lys
841/281	ATT	GAA	AAA	GTC	CTG	CAG	CAG	GGA	GAT	ATT	GGA	GAC	TGT	GCA	GAG	CCC	TAC	ACG	GTT	ATC
	ile	glu	lys	val	leu	gln	gln	gly	asp	ile	gly	asp	cys	ala	glu	pro	tyr	thr	val	ile
901/301	AAA	GAA	AGT	GAT	GCT	GGA	AAG	AGT	AAA	GAA	AAG	ATT	GAA	AAA	CTA	AAA	CTC	CAA	GCT	GAA
	lys	glu	ser	asp	gly	gly	lys	ser	lys	glu	lys	ile	glu	lys	leu	lys	leu	gln	ala	glu

1021/341

TCA AGC TTC TTC AAT GTC TCC ACC CTT GAG
 ser ser phe phe asn val ser thr leu glu
 1081/361
 GGG AGA AGC CCA GTG GGT GAA CGG AGG ACA
 gly arg ser pro val gly glu arg arg thr
 1141/381
 GCC CTC TCC TTG GAG GAA AAT GGG GTT GGA
 ala leu ser leu glu glu asn gly val gly
 1201/401
 AGC AGC TTT TTC AAG CAG GAA GGA GAT CGC
 ser ser phe phe lys gln glu gly asp arg
 1261/421
 GCT GAC TAC AAA AGA TCA TCA TCC TTA CAG
 ala asp tyr lys arg ser ser ser leu gln
 1321/441
 AGA CTG GAG ATT TCT ACA GCT CCA GAG ATC
 arg leu glu ile ser thr ala pro glu ile
 1381/461
 CCC GTG AAA CCC TTT CCT GAA AAC CGG ACA
 pro val lys pro phe pro glu asn arg thr
 1441/481
 ACA CGA GAA GTA TAT GTC CCT CAC ACT GTG
 thr arg glu val tyr val pro his thr val
 1501/501
 AGG CTG AAC TTT GTA AAC AAA CTA GCA TCA
 arg leu asn phe val asn lys leu ala ser
 1561/521
 ATG TGT GGA GAA GAT GCT AGC AAT GCG ATG
 met cys gly glu asp ala ser asn ala met
 1621/541
 GAA TTT CTG CAG GAA GTG TAC ACA GCT GTT
 glu phe leu gln glu val tyr thr ala val
 1681/561
 GAA GAA GTG AAA ATT AAG CTC CCC GCT AAG
 glu glu val lys ile lys leu pro ala lys
 1741/581
 TTC TAC CAT ATC AGC TGT CAG CAG AAG CAA
 phe tyr his ile ser cys gln gln lys gln
 1801/601
 TCA TGG CTG CCA ATT CTC TTA AAT GAA CGT
 ser trp leu pro ile leu leu asn glu arg
 1861/621
 GCC TTG GAA AAA TTG CCA CCC AAC TAC TCC
 ala leu glu lys leu pro pro asn tyr ser
 1921/641
 AAT CCT CCC ATT AAG TGG GCT GAA GGA CAT
 asn pro pro ile lys trp ala glu gly his
 1981/661
 GTT TCT TCT GTA CAC ACC CAG GAC AAC CAC
 val ser ser val his thr gln asp asn his
 2041/681
 CTG GAG AGC CAG GTG ACC TTC CCC ATC CGC
 leu glu ser gln val thr phe pro ile arg

1051/351

AGG GAG GTA ACT GAT GTG GAC TCT GTG GTT
 arg glu val thr asp val asp ser val val
 1111/371
 TTG GCC CAA TCT AGA AGG CTT TCT GAA AGA
 leu ala gln ser arg arg leu ser glu arg
 1171/391
 TCC AAC TTC AAA ACC TCC ACT CTG AGC GTT
 ser asn phe lys thr ser thr leu ser val
 1231/411
 CTT AGC GAT GAA GAC TTA TTC AAG TTT TTA
 leu ser asp glu asp leu phe lys phe leu
 1291/431
 AGA CGA GTC AAG TCA ATT CCA GGC TTG CTA
 arg arg val lys ser ile pro gly leu leu
 1351/451
 ATC AAT TGC TGT CTG ACT CCT GAA ATG CTG
 ile asn cys cys leu thr pro glu met leu
 1411/471
 CGC CCG CAC AAA GAG ATT TTG GAA TTT CCA
 arg pro his lys glu ile leu glu phe pro
 1471/491
 TAC AGA AAC CTT CTC TAT GTC TAC CCA CAG
 tyr arg asn leu leu tyr val tyr pro gln
 1531/511
 GCC CGG AAC ATT ACA ATA AAG ATC CAG TTT
 ala arg asn ile thr ile lys ile gln phe
 1591/531
 CCG GTC ATC TTT GGA AAA TCC AGC GGG CCT
 pro val ile phe gly lys ser ser gly pro
 1651/551
 ACA TAC CAT AAT AAG TCT CCT GAC TTT TAT
 thr tyr his asn lys ser pro asp phe tyr
 1711/571
 CTC ACA GTA AAT CAC CAC CTC CTG TTC ACC
 leu thr val asn his his leu leu phe thr
 1771/591
 GGA GCC TCC GTG GAA ACT CTC CTG GGA TAT
 gly ala ser val glu thr leu leu gly tyr
 1831/611
 CTT CAA ACT GGA TCC TAC TGT CTC CCA GTT
 leu gln thr gly ser tyr cys leu pro val
 1891/631
 ATG CAT TCT GCT GAG AAA GTC CCA TTA CAG
 met his ser ala glu lys val pro leu gln
 1951/651
 AAG GGA GTA TTT AAT ATT GAA GTG CAA GCT
 lys gly val phe asn ile glu val gln ala
 2011/671
 CTG GAG AAG TTC TTC ACC CTC TGC CAC TCC
 leu glu lys phe phe thr leu cys his ser
 2071/691
 GTG CTG GAT CAG AAA ATC AGC GAG ATG GCG
 val leu asp gln lys ile ser glu met ala

2161/721

GTG CTC TTC CTG CAC CTG GTG CTG GAC AAG
 val leu phe leu his leu val leu asp lys
 2221/741
 ATC GCT GGC CAG ACA GCC AAC TTC TCC CAG
 ile ala gly gln thr ala asn phe ser gln
 2281/761
 AAC AGT CTG CAC AAC AGC AAG GAC CTG AGC
 asn ser leu his asn ser lys asp leu ser
 2341/781
 GCT TCC TAC GTG CAC TAC GTC TTC CGC CTG
 ala ser tyr val his tyr val phe arg leu
 2401/801
 GGC GCT CCC ACT GCC CTC CTA GAC CCT CGG
 gly ala pro thr ala leu leu asp pro arg
 2461/821
 GCT GCT GTG AGT TCA AAG CTG CTG CAG GCC
 ala ala val ser ser lys leu leu gln ala
 2521/841
 GCG GGG ACA CAC TCC GCA GCA GAC GAG GAA
 ala gly thr his ser ala ala asp glu glu
 2581/861
 GAT CGC AAC TGC AGC CGA ATG TCT TAC TAT
 asp arg asn cys ser arg met ser tyr tyr
 2641/881
 CCT GCA GCC CCA AGG CCA GCC AGC AAA AAG
 pro ala ala pro arg pro ala ser lys lys
 2701/901
 GTG GTC AGC ACC GGA ATG GTG AAA AGC ATG
 val val ser thr gly met val lys ser met
 2761/921
 GAC AGT TTT CGG AGG ACT CGT TTT TCT GAC
 asp ser phe arg arg thr arg phe ser asp
 2821/941
 AAT GTG GTC ACC TCG GAA ATT GCA GCC CTT
 asn val val thr ser glu ile ala ala leu
 2881/961
 GCG GAA AAG ATG AAC ATC AGC CTG GCT TTC
 ala glu lys met asn ile ser leu ala phe
 2941/981
 CGG GGC TTT GTG TTT AAC CTC ATC AGA CAT
 arg gly phe val phe asn leu ile arg his
 3001/1001
 AAC CTT CCA ACG CTC ATT TCC ATG AGG CTA
 asn leu pro thr leu ile ser met arg leu
 3061/1021
 CAT TAC CTC AAT CTG AAC CTT TTT TTT ATG
 his tyr leu asn leu asn leu phe phe met
 3121/1041
 CCT TCC ATA TCT TCC CAG AAC TCA AGC TCC
 pro ser ile ser ser gln asn ser ser ser
 3181/1061
 AGC ATG TTC GAT CTG ACT TCC GAG TAC CGC

2191/731

CTC TTC CAG CTG TCC GTG CAG CCC ATG GTC
 leu phe gln leu ser val gln pro met val
 2251/751
 TTT GCC TTC GAG TCC GTG GTG GCC ATC GCC
 phe ala phe glu ser val val ala ile ala
 2311/771
 AAG GAC CAG CAT GGG AGG AAC TGC CTG CTG
 lys asp gln his gly arg asn cys leu leu
 2371/791
 CCA GAG GTG CAA AGG GAT GTG CCC AAG TCA
 pro glu val gln arg asp val pro lys ser
 2431/811
 AGC TAC CAC ACG TAT GGC CGC ACA TCA GCT
 ser tyr his thr tyr gly arg thr ser ala
 2491/831
 CGG GTG ATG AGC AGC AGT AAC CCA GAC CTC
 arg val met ser ser ser asn pro asp leu
 2551/851
 GTG AAG AAC ATC ATG TCT TCA AAG ATC GCC
 val lys asn ile met ser ser lys ile ala
 2611/871
 TGC TCT GGC AGT AGT GAT GCT CCA AGT TCA
 cys ser gly ser ser asp ala pro ser ser
 2671/891
 CAT TTC CAT GAG GAG CTT GCC CTT CAG ATG
 his phe his glu glu leu ala leu gln met
 2731/911
 GCC CAG CAC GTA CAT AAC ATG GAC AAA CGG
 ala gln his val his asn met asp lys arg
 2791/931
 CGT TTC ATG GAT GAC ATA ACT ACT ATT GTT
 arg phe met asp asp ile thr thr ile val
 2851/951
 TTA GTA AAA CCA CAG AAG GAA AAT GAA CAG
 leu val lys pro gln lys glu asn glu gln
 2911/971
 TTC TTG TAT GAC CTT CTC TCC CTC ATG GAT
 phe leu tyr asp leu leu ser leu met asp
 2971/991
 TAT TGC AGC CAG CTG TCA GCC AAG CTC AGT
 tyr cys ser gln leu ser ala lys leu ser
 3031/1011
 GAG TTC CTG AGA ATC CTC TGT AGC CAT GAG
 glu phe leu arg ile leu cys ser his glu
 3091/1031
 AAT GCT GAT ACT GCT CCA ACA TCT CCT TGT
 asn ala asp thr ala pro thr ser pro cys
 3151/1051
 TGC TCC AGC TTC CAG GAC CAG AAG ATC GCC
 cys ser ser phe gln asp gln lys ile ala
 3211/1071
 CAG CAG CAC TTC CTC ACC GGG CTC CTC TTC
 gln gln his phe leu thr gly leu leu phe

3301/1101

GCT GTC AGT GCA ATT CAC AGC CTG CTA AGT
ala val ser ala ile his ser leu leu ser

3361/1121

CCA GAG GTG AAG GTC AAA ATC GCC GCC CTT
pro glu val lys val lys ile ala ala leu

3421/1141

GCT TTG CCA CAG CTC TGT GAC TTT ACA GTT
ala leu pro gln leu cys asp phe thr val

3481/1161

TCG GAT GAA GAA CAA GAA GGA GCC GGT GCC
ser asp glu glu gln glu gly ala gly ala

3541/1181

GGG AAT AAT TTC AAT TTG AAA ACA AGT GGA
gly asn asn phe asn leu lys thr ser gly

3601/1201

TAC AAC ATG CTG AAC GCG GAC ACT ACT CGC
tyr asn met leu asn ala asp thr thr arg

3661/1221

AAA AAT GCT GAT CAG AGC CTC ATT AGG AAG
lys asn ala asp gln ser leu ile arg lys

3721/1241

AAC AGG ATT TTA GAT CTA CTT TTC ATC TGT
asn arg ile leu asp leu leu phe ile cys

3781/1261

AGT TCT GAC AAA GTC AGT ACC CAA GTC CTG
ser ser asp lys val ser thr gln val leu

3841/1281

GAA GAG GCT TTG CTG CGT GGG GAA GGG GCC
glu glu ala leu leu arg gly glu gly ala

3901/1301

GGG AAC GAC CGA TTT CCA GGC CTA AAT GAA
gly asn asp arg phe pro gly leu asn glu

3961/1321

TGG CGG CAA GCT AAT GAG AAG CTA GAT AAA
trp arg gln ala asn glu lys leu asp lys

4021/1341

ATC AGT GGC AAT CTG GCT ACA GAA GCA CAT
ile ser gly asn leu ala thr glu ala his

4081/1361

ATC CAG GCG AGC TCG GCT CTG GAC TGT AAA
ile gln ala ser ser ala leu asp cys lys

4141/1381

CTG GTG AAT TCT CTG AAC TGT GAT CAG AGT
leu val asn ser leu asn cys asp gln ser

4201/1401

CTC CGT GCT CTC ATC GCC AAG TTT GGA GAC
leu arg ala leu ile ala lys phe gly asp

4261/1421

TTC GAC CTA TGT CAC CAA GTC CTG CAC CAC
phe asp leu cys his gln val leu his his

4321/1441

CAA GCC TGT GCC ACC CTT TAC CTC CTC ATG
gln ala cys ala thr leu tyr leu leu met

3331/1111

TCT CAC GAC CTG GAC CCA CGC TGT GTC AAA
ser his asp leu asp pro arg cys val lys

3391/1131

TAC CTA CCT TTA GTT GGC ATC ATT TTG GAT
tyr leu pro leu val gly ile ile leu asp

3451/1151

GCA GAT ACT CGC AGA TAC CGC ACC AGT GGC
ala asp thr arg arg tyr arg thr ser gly

3511/1171

ATT AAC CAG AAT GTG GCT CTG GCC ATA GCA
ile asn gln asn val ala leu ala ile ala

3571/1191

ATA GTG CTG TCT TCC TTG CCC TAT AAG CAG
ile val leu ser ser leu pro tyr lys gln

3631/1211

AAC CTC ATG ATC TGC TTC CTC TGG ATC ATG
asn leu met ile cys phe leu trp ile met

3691/1231

TGG ATT GCT GAC CTG CCA TCA ACG CAG CTC
trp ile ala asp leu pro ser thr gln leu

3751/1251

GTG TTA TGT TTT GAG TAT AAG GGA AAA CAG
val leu cys phe glu tyr lys gly lys gln

3811/1271

CAG AAG TCA AGG GAT GTC AAG GCC CGG CTG
gln lys ser arg asp val lys ala arg leu

3871/1291

AGA GGG GAG ATG ATG CGC CGG GCT CCA
arg gly glu met met arg arg arg ala pro

3931/1311

AAT TTG AGA TGG AAG AAA GAG CAG ACA CAT
asn leu arg trp lys lys glu gln thr his

3991/1331

ACA AAG GCC GAG TTA GAT CAA GAA GCC TTG
thr lys ala glu leu asp gln glu ala leu

4051/1351

TTA ATC ATC CTG GAT ATG CAG GAA AAC ATT
leu ile ile leu asp met gln glu asn ile

4111/1371

GAC AGC CTG CTG GGA GGT GTT CTG AGG GTG
asp ser leu leu gly gly val leu arg val

4171/1391

ACC ACC TAC CTG ACT CAC TGC TTT GCA ACA
thr thr tyr leu thr his cys phe ala thr

4231/1411

TTA CTC TTC GAA GAG GAG GTG GAA CAG TGT
leu leu phe glu glu glu val glu gln cys

4291/1431

TGC AGC AGC AGC ATG GAT GTC ACC CGG AGC
cys ser ser ser met asp val thr arg ser

4351/1451

AGG TTC AGT TTT GGA GCC ACC AGT AAT TTT
arg phe ser phe gly ala thr ser asn phe

4441/1481

TTT AAT GAA GAG CAC CTG AGA AGA TCC TTG
 phe asn glu glu his leu arg arg ser leu
 4501/1501
 ACA GCC ATG CAG ATG ACT CCT TTT CCC ACC
 thr ala met gln met thr pro phe pro thr
 4561/1521
 AGC ATC TTA TAT GAC ACA GTG AAA ATG AGG
 ser ile leu tyr asp thr val lys met arg
 4621/1541
 GAT CTC ATG TAC AGA ATT GCC AAG AGT TAC
 asp leu met tyr arg ile ala lys ser tyr
 4681/1561
 CTC CAG AAC ATG GCA GAG AAA CAC ACC AAG
 leu gln asn met ala glu lys his thr lys
 4741/1581
 CTG GTG CAC GCC GCT GCG TTA GTG GCT GAG
 leu val his ala ala ala leu val ala glu
 4801/1601
 CTG CCC GTG GGC AGT GTC AGC TTC CAG AAT
 leu pro val gly ser val ser phe gln asn
 4861/1621
 GTC TCT GAG GAC ACC CTG TCA CCT GAC GAG
 val ser glu asp thr leu ser pro asp glu
 4921/1641
 GAG AGT GGC CTG GTA GGC CTC CTG GAG CAG
 glu ser gly leu val gly leu leu glu gln
 4981/1661
 TAT GAG ACA GTT AAT GAG GTC TAC AAG CTG
 tyr glu thr val asn glu val tyr lys leu
 5041/1681
 TTC CGG AAG CTG ACA CTC ACT CAC AGC AAG
 phe arg lys leu thr leu thr his ser lys
 5101/1701
 AAG GAT CAT AAG AGA ATG TTT GGA ACC TAC
 lys asp his lys arg met phe gly thr tyr
 5161/1721
 GGG GAT TTG GAT GAA CAG GAG TTT GTC TAC
 gly asp leu asp glu gln glu phe val tyr
 5221/1741
 ATC TCA CAT AGA CTA GAG GCA TTT TAT GGT
 ile ser his arg leu glu ala phe tyr gly
 5281/1761
 ATT AAA GAC TCC ACT CCT GTG GAC AAA ACC
 ile lys asp ser thr pro val asp lys thr
 5341/1781
 ATC ACT TTT GTG GAG CCC TAC TTT GAT GAG
 ile thr phe val glu pro tyr phe asp glu
 5401/1801
 GAG AAG AAT TTC AAC CTC CGG AGG TTC ATG
 glu lys asn phe asn leu arg arg phe met
 5461/1821
 CCT CGG GGA GAG CTG CAT GAG CAG TAC AGA
 pro arg glu glu leu his glu glu tyr arg

4471/1491

AGG ACA ATT TTG GCC TAT TCA GAA GAG GAC
 arg thr ile leu ala tyr ser glu glu asp
 4531/1511
 CAG GTG GAG GAA CTT CTC TGT AAT CTG AAT
 gln val glu glu leu leu cys asn leu asn
 4591/1531
 GAA TTT CAG GAA GAT CCT GAG ATG CTT ATG
 glu phe gln glu asp pro glu met leu met
 4651/1551
 CAG GCA TCT CCT GAT CTG CGG CTG ACC TGG
 gln ala ser pro asp leu arg leu thr trp
 4711/1571
 AAG AAG TGC TAC ACG GAG GCT GCC ATG TGC
 lys lys cys tyr thr glu ala ala met cys
 4771/1591
 TAT CTG AGC ATG CTG GAG GAC CAC AGC TAC
 tyr leu ser met leu glu asp his ser tyr
 4831/1611
 ATT TCT TCC AAT GTG CTG GAG GAG TCT GTG
 ile ser ser asn val leu glu glu ser val
 4891/1631
 GAT GGG GTG TGC GCA GGC CAG TAC TTC ACC
 asp gly val cys ala gly gln tyr phe thr
 4951/1651
 GCC GCG GAG CTC TTC AGC ACG GGA GGC TTA
 ala ala glu leu phe ser thr gly gly leu
 5011/1671
 GTC ATC CCC ATC CTA GAA GCG CAT CGA GAA
 val ile pro ile leu glu ala his arg glu
 5071/1691
 CTG CAG AGA GCC TTC GAC AGC ATC GTT AAC
 leu gln arg ala phe asp ser ile val asn
 5131/1711
 TTC CGA GTT GGT TTC TTT GGA TCC AAA TTT
 phe arg val gly phe phe gly ser lys phe
 5191/1731
 AAA GAG CCT GCA ATT ACC AAG CTT CCT GAG
 lys glu pro ala ile thr lys leu pro glu
 5251/1751
 CAA TGT TTT GGT GCA GAA TTT GTG GAA GTG
 gln cys phe gly ala glu phe val glu val
 5311/1771
 AAG TTG GAT CCT AAC AAG GCC TAC ATA CAG
 lys leu asp pro asn lys ala tyr ile gln
 5371/1791
 TAT GAG ATG AAA SAC AGG GTC ACA TAC TTT
 tyr glu met lys asp arg val thr tyr phe
 5431/1811
 TAC ACC ACC CCG TTC ACC CTG GAG GGG CGG
 tyr thr thr pro phe thr leu glu gly arg
 5491/1831
 AGG AAC ACA GTC CTG ACC ACT ATG CAC GCC
 arg asn thr val leu thr thr met his ala

5581/1861

ATT GAA GTT GCC ATT GAA GAC ATG AAG AAG AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC
 ile glu val ala ile glu asp met lys lys lys thr leu gln leu ala val ala ile asn

5641/1881

CAG GAG CCG CCT GAT GCA AAG ATG CTT CAG ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT
 gln glu pro pro asp ala lys met leu gln met val leu gln gly ser val gly ala thr

5701/1901

GTA AAT CAG GGA CCA CTG GAA GTA GCC CAA GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA
 val asn gln gly pro leu glu val ala gln val phe leu ala glu ile pro ala asp pro

5761/1921

AAA CTC TAT CGA CAT CAC AAC AAG TTG AGG TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT
 lys leu tyr arg his his asn lys leu arg leu cys phe lys glu phe ile met arg cys

5821/1941

GGT GAA GCT GTA GAG AAA AAC AAG CGT CTC ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG
 gly glu ala val glu lys asn lys arg leu ile thr ala asp gln arg glu tyr gln gln

5881/1961

GAA CTC AAA AAG AAC TAT AAC AAG CTA AAA GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA
 glu leu lys lys asn tyr asn lys leu lys glu asn leu arg pro met ile glu arg lys

5941/1981

ATT CCA GAA CTG TAC AAG CCA ATA TTC AGA GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC
 ile pro glu leu tyr lys pro ile phe arg val glu ser gln lys arg asp ser phe his

6001/2001

AGA TCT AGT TTC AGG AAA TGT GAA ACC CAG TTG TCA CAG GGC AGC TAA
 arg ser ser phe arg lys cys glu thr gln leu ser gln gly ser OCH

5611/1871

AAG ACC CTG CAG TTA GCA GTT GCC ATT AAC
 lys thr leu gln leu ala val ala ile asn

5671/1891

ATG GTG CTG CAA GGC TCT GTG GGA GCT ACT
 met val leu gln gly ser val gly ala thr

5731/1911

GTG TTT TTG GCT GAA ATT CCT GCT GAT CCA
 val phe leu ala glu ile pro ala asp pro

5791/1931

TTA TGC TTT AAG GAA TTC ATC ATG AGA TGT
 leu cys phe lys glu phe ile met arg cys

5851/1951

ATC ACG GCA GAC CAG AGG GAA TAT CAG CAG
 ile thr ala asp gln arg glu tyr gln gln

5911/1971

GAG AAC CTC AGG CCA ATG ATC GAG CGG AAA
 glu asn leu arg pro met ile glu arg lys

5971/1991

GTT GAG AGT CAA AAG AGG GAC TCC TTC CAC
 val glu ser gln lys arg asp ser phe his

6031/2011

TTG TCA CAG GGC AGC TAA
 leu ser gln gly ser OCH

GAAAAGCCATCTTCATTCGTGGAGACTGTGGCCCTGCAACCCTGGAGAAGGACTTGCTGGTACTTAAAAATGGGACATT
 TGCCACCCAGGACTGACTGTACACTCCCTGATCAGCCAGCACTCTGGAAGCTTTGGGATCCCAGGAACCATGGAATTATT
 CCCAAATGGACTCTGACCAGATTTTTGCCATACTGGGGGGTGGCGGGATGGAGGATGGGTACTCAGGCATGACTGCGTAT
 TTATTAAAGTGTGTTTTCCACAATGTACCAACAAGGCATAAGCAGCTTCTCCTGCTGACTGGCCAATCACTGCCCATC
 TGAGAGATGATTTCTCTGGCCCCATATTTGAATTTATTGGAGTAACCTCAAATTGCCTGAGGAAAAATGGAAAAATATCC
 ACCAGTCGATTCAAACTGAATTTCACTCTTTATAGGAAGGCAGGGCAAACCTGTAGGAGTACGAAACATTTTCAATAAAT
 CTACAAAGGGAAGCCTTACTACAATTCAAAAATCATCATGTTGGAAATTTGGGAGGAGATTATTTGTGAACCTGTTAC
 CCTTTTGGTAATGGTGGACTAATTGCTGTATAGTTATTTTGTTTTATTATTACTGTTACATTAATTTAACATGCATTTA
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 CACTTAAATGGAAACAATTTCTCCGATAATGCTTTTGCTTTTTTCTTATGTCACTCTTGTGTACTATCTATTTTCTCCTC
 TCTGGGACCAAGTTTCTTTTATAAAGCAATAATATCTCTGTTTTTCATTTTCAGAACATTGTGCTGTCTGTCAGCATATGT
 ATATCAGCTACAAAATATATTCAACTTTGACTTCTTTTGACAAAGGACTTTAGGAAAAGGAGGAACAAAGACATTATTTG
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 AAAAAAAAAAACTCG

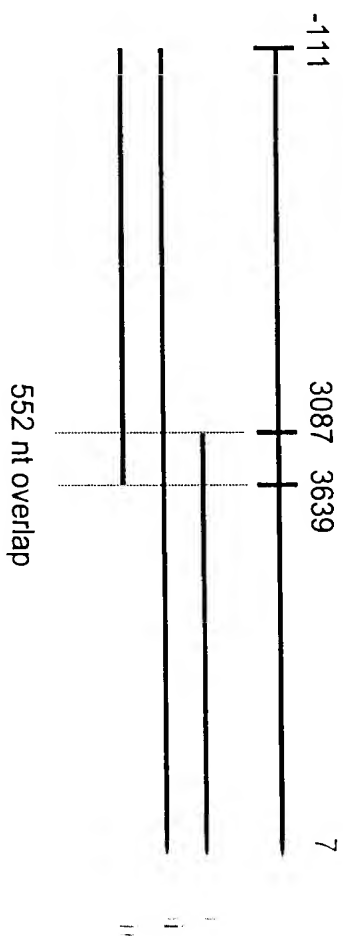
A. Allelic variations: single nucleotide changes (polymorphism) between CLASP-5 cDNA isoforms

Isoform	Nucleotide(s)	Consequence
1	1727	C to T change; mis-sense mutation changing codon from alanine to valine
2	1749	A to G change; silent mutation
3	2277	G to C change; silent mutation
4	2853	C to T change; silent mutation
5	3427	A to G change; mis-sense mutation changing codon from lysine to glutamic acid
6	3777	C to T change; silent mutation

B. Alternative splices

Isoform	Difference	Nucleotide(s)	Consequence
1	exon deletion	1806-1944	premature, in-frame stop codon leading to the production of a truncated, most likely soluble protein
2	exon insertion	between 2857 and 2858	additional, in-frame 48 nucleotide exon that contains a stop codon at the second codon, which would lead to a truncated, most likely soluble protein

nucleotide numbering
as in Figure 6A



1st partial exon (nucleotides 3793 to 3952)

CCAGCTGTCAGCCAAGCTCAGTAACCTTCCAACGCTCATTTCATGAGGCTAG
AGTTCCTGAGAATCCTCTGTAGCCATGAGCATTACCTCAATCTGAACCTTTTT
TTTATGAATGCTGATACTGCTCCAACATCTCCTTGTCTTCCATATCTTCCCAG
GTAATAAAAAGAATTATTTAACTAAAAGAATTATTCAAGCTAT

2nd exon (nucleotides 5809 to 5948)

GCTCATAAAATGGCTCCTTACGTTTCTGTAGAACTCAAGCTCCTGCTCCAGCT
TCCAGGACCAGAAGATCGCCAGCATGTTTCGATCTGACTTCCGAGTACCGCCA
GCAGCACTTCCTCACCGGGCTCCTCTTACAGAACTGGCTGCTGCCCTGGATG
CCGAAGGGGAAGGGTATGTTTCTGGCATTTAAAATGGAAGATGAAGC

3rd exon (nucleotides 13662 to 13831)

CATAACCTCTTGATTCTGTGTTTGCCAACAGAATCAGCAAAGTACAAAGG
AAAGCTGTCAAGTGCAATTCACAGCCTGCTAAGTTCTCACGACCTGGACCCAC
GCTGTGTCAAACCAGAGGTGAAGGTCAAAATCGCCGCCCTTTACCTACCTTTA
GTTGGCATCATTTTGGATGCTTTGCCACAGCTCTGTGACTTTACAGGTAATGG
CCCTTCTGTTTCTTTCTTGGATTG

4th exon (nucleotides 16948 to 17087)

TGTTTGACTTGACATCACAAACGATGTTTTATTGCAGTTGCAGATACTCGCA
GATACCGCACCAGTGGCTCGGATGAAGAACAAGAAGGAGCCGGTGCCATTA
ACCAGAAATGTGGCTCTGGCCATAGCAGGGAATAATTTCAATTTGAAAACAAG
TGGAATAGTGCTGTCTTCCTTGGTATGTTGGTGCACATGTGTCTGGTTGATTTT
TCAT

5th exon (nucleotides 19281 to 19463)

TGGCCTCCATCCCCCAATCTGCCTCCCTTCAGCCCTATAAGCAGTACAACATG
CTGAACGCGGACACTACTCGCAACCTCATGATCTGCTTCCTCTGGATCATGAA
AAATGCTGATCAGAGCCTCATTAGGAAGTGGATTGCTGACCTGCCATCAACG
CAGCTCAACAGGATTTTAGATCTACTTTTCATCTGTGTGTTATGTTTTGAGTAT
AAGGTAAGTCTGGAGTGGCACAACCTTATACCAGC

6th exon (nucleotides 19829 to 19958)

CACCAAAGGACATGTCCTCCTACCTCTGTCTTGTCCAGGGAAAACAGAGTTCT
GACAAAGTCAGTACCCAAGTCTGCAGAAGTCAAGGGATGTCAAGGCCCGG
CTGGAAGAGGCTTTGCTGCGTGGGGAAGGGGCCAGAGGGGAGATGATGCGC

7th exon (nucleotides 20928 to 21015)

TCAAATTCTCATCATGCAATTTCTTAACTCCTAGGGAACGACCGATTTCCAGGC
TAAATGAAAATTTGAGATGGAAGAAAGAGCAGACACATTGGCGGCAAGCT
AATGAGAAGCTAGATAAGTGAGTCACTCGGCAACTTTCTGCTACTTTTACCT

8th exon (nucleotides 25765 to 25861)

GCTTTAATTTGACCTCTTGTTGTTTCTAGAACAAAGGCCGAGTTAGATCAAG
AAGCCTTGATCAGTGGCAATCTGGCTACAGAAGCACATTTAATCATCTGGA
TATGCAGGAAAACATTATCCAGGTGAGGAAAACAAACACCCAATCTGATTG

9th exon (nucleotides 27242 to 27376)

GGATTCAATGATGCTGTTCTTCCATTCCCCAGGCGAGCTCGGCTCTGGACTG
TAAAGACAGCCTGCTGGGAGGTGTTCTGAGGGTGCTGGTGAATTTCTCTGAAC
TGTGATCAGAGTACCACCTACCTGACTCACTGCTTTGCAACACTCCGTGCTCT
CATCGCCAAGGTAAACTTGGGATGCTTGTTTTCTTCTCTTAATT

10th exon (nucleotides 28582 to 28734)

AGTGATGCCTAATGGCCCTTTATGTCTCTCCTAGTTTGGGAGACTTACTCTTCG
AAGAGGAGGTGGAACAGTGTTTCGACCTATGTCACCAAGTCCTGCACCACTG
CAGCAGCAGCATGGATGTCACCCGGAGCCAAGCCTGTGCCACCCCTTACCTC
CTCATGAGGTTTCACTTTTGGAGCCACCAAGTGTAAGAGTTCAAACCAAGCTGAG
TGACCTGGAATCAG

11th exon (nucleotides 31046 to 31204)

TTACTTCATCTTTTTTTTTTTTTTCACTGATGCAGAAATTTTGCAAGAGTAAAGA
TGCAAGTAACCATGTCCCTGGCATCTTTGGTGGGAAGAGCACCAGACTTTAA
TGAAGAGCACCTGAGAAGATCCTTGAGGACAATTTTGGCCTATTCAGAAGAG
GACACAGCCATGCAGATGACTCTTTTCCCACCCAGGTACACCGAAGCACAT
ACCTTGCTCATGCATGAGT

12th exon (nucleotides 32755 to 32855)

AGCTAAGATTATTTTGAGGCTTACACTTTTTGCAGGTGGAGGAACTTCTCTGT
AATCTGAATAGCATCTTATATGACACAGTGAAAATGAGGGAATTTAGGAAG
ATCCTGAGATGCTTATGGATCTCATGTACAGGTAAGCTTTCCTGACACACTCA
AGGGACACCATTT

13th exon (nucleotides 33663 to 33855)

TCCTCAAAACTACTTCTCACTCAATCTGTCTTCAGAATTGCCAAGAGTTACCA
GGCATCTCCTGATCTGCGGCTGACCTGGCTCCAGAACATGGCAGAGAAACAC
ACCAAGAAGAAGTGCTACACGGAGGCTGCCATGTGCCTGGTGCACGCCGCTG
CGTTAGTGGCTGAGTATCTGAGCATGCTGGAGGACCACAGCTACCTGCCCGT
GGGCAGTGTACAGCTTCCAGGTAGGGTGTGTGCAGCTTTCCCTTAGAGCAGTG
GTTC

CTGTTCTCCAGGCTTATACTGTGGTCTCTTTTCAGAATATTTCTTCCAATGTGCT
GGAGGAGTCTGTGGTCTCTGAGGACACCTGTACCTGACGAGGATGGGGTG
TGCGCAGGCCAGTACTTCACCGAGAGTGGCCTGGTAGGCCTCCTGGAGCAGG
CCGCGGAGCTCTTCAGCACGGTCAGTGCCAGAGGGCATCCCGGGGCCTGGC
C

15th exon (nucleotides 40166 to 40297)

AATTCTCTCTGATGCTCTTCTCCTCTTTCCAAGGGAGGCTTATATGAGACAGT
TAATGAGGTCTACAAGCTGGTCATCCCCATCCTAGAAGCGCATCGAGAATTC
CGGAAGCTGACACTCACTCACAGCAAGCTGCAGAGAGCCTTCGACAGCATCG
TTAACAAGGTAGCCGGGGAGCCTGGCTGGCAGGTCTTGTTAC

16th exon (nucleotides 40755 to 40889)

TAAGGAGAGCTTTTTATATTTTGTTCCTCAGGATCATAAGAGAATGTTTGGAA
CCTACTTCCGAGTTGGTTTCTTTGGATCCAAATTTGGGGATTGGATGAACAG
GAGTTTGTCTACAAAGAGCCTGCAATTACCAAGCTTCCTGAGATCTCACATAG
ACTAGAGGTAAGAAAAGTGATTCTGTGCGCCTGACCTGGTACACTTTAC

17th exon (nucleotides 42307 to 42396)

AACCTTTATAAACTGTTGGTCTTCTTACCTAGGCATTTTATGGTCAATGTTTT
GGTGCAGAAATTTGTGGAAGTGATTAAAGACTCCACTCCTGTGGACAAAACCA
AGTTGGATCCTAACAAAGGTATACAAAAATTTACAAAACTAACCATCAAGC

18th exon (nucleotides 45250 to 45486)

TCTTCTCCCTCCGTGCCTTTTCCCCCTTAGGCCTACATACAGATCACTTTTGTG
GAGCCCTACTTTGATGAGTATGAGATGAAAGACAGGGTCACATACTTTGAGA
AGAATTTCAACCTCCGGAGGTTTCATGTACACCACCCCGTTACCCCTGGAGGG
GCGGCCTCGGGGAGAGCTGCATGAGCAGTACAGAAGGAACACAGTCCTGAC
CACTATGCACGCCTTCCCCTACATCAAGACCAGGATCAGCGTCATCCAGAAG
GAGGAGGTAATGCACCCAAGGGATTGGCCACCACTGGATGAGT

19th exon (nucleotides 48664 to 48807)

ACAGTGACTTCCCTATGTTTACGTCTCATGTTTCAGTTTGTGTTTGACACCGATTG
AAGTTGCCATTGAAGACATGAAGAAGAAGACCCTGCAGTTAGCAGTTGCCAT
TAACCAGGAGCCGCCTGATGCAAAGATGCTTCAGATGGTGCTGCAAGGCTCT
GTGGGAGCTACTGTAAATCAGGTAAGCAAAACCAGAGGTGGCAGTCTCT

20th exon (nucleotides 50892 to 50998)

TATATTCTTTTTTTTTTTTTTTTTTTTTTTTCCCACCAGGGACCACTGGAAGTAGC
CCAAGTGTTTTGGCTGAAATTCCTGCTGATCCAAAACCTCTATCGACATCACA
ACAAGTTGAGGTTATGCTTTAAGGAATTCATCATGAGGTAAGAAGGAAAATG
GCTGGGAATTCAGTAGAG

21st exon (nucleotides 62398 to 62568)

TCAAAAAGAACTATAACAAGCTAAAAGAGAACCTCAGGCCAATGATCGAGC
GGAAAAATTCCAGAACTGTACAAGCCAATATTCAGAGTTGAGAGTCAAAAGAG
GTAAGAACAGGGCAGAGGAGGCCTCTTCTGTGGGAT

22nd exon (nucleotides 63040 to 63294)

CCTCCCTCTCTTTTCTTAATTTACAGGGACTCCTTCCACAGATCTAGTTTCAGGA
AATGTGAAACCCAGTTGTACAGGGCAGCTAAGAAAAGCCATCTTCATTTCGT
GGAGACTGTGGCCCTGCAACCCTGGAGAAGGACTTGCTGGTACTTAAAAAAT
GGGACATTTGCCACCCAGGACTGACTGTACACTCCCTGATCAGCCAGCACTC
TGGAAGCTTTGGGATCCCAGGAACCATGGAATTATTCCTCAATGGACTCTGA
CCAGATTTTTGCCATACTGGGGGGTGGCGGGATGGAGGATGGGTACTCAGGC
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AAGCAGCTTCTCCTGCTGACTGGCCAATCACTGCCCATCTGAGAGATGATTC
CTCTGGCCCATATTTGAATTTATTGGAGTAACTCAAATTCCTGAGGAAAAAT
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9101 AGATAAAAAATATAATATTCCATTATCTCTCTCAGTTACAGGCCCCCTCAAGTAACCACTATTCTGACTCTTATTATTAGAAATTAATA
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 9283 CAACTGTATGTCATATTCCTTTGTCTACTATAATTTCTCTTCTGTAAATTGACATTTGGGCTGCTTTCTATTTGTGGGTATTTGGGTATTAT
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 9556 AGCAACAAGTCAAAGCAGGAAGATGGCAGGGAATAACAAAGGTGATAGCCAAAATAAATGAAATAAAGAAATAGAAAAACAATCACGGAAA
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 13014 AAAAAAAAAAAGTTAAACAGACAGTTTACCATACAAGCCAGCAATGTACTCTGAGGTATGTACCAAGAAAAAGTAAACCTTAAACCTGT
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13651 TGTGCCAACAGAATCAGCAAAGTACAAAGGAAAGCTGTCACTGCAATTCACAGCCTGCTAAGTTCTCACGACCTGGACCCACGCTGTGTCA
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 39131 CTCAGTGATCTGCCATCTTGGCTCCCAAAGTCTGGAACCTACAGGTGTGAGCCACCACGCCCACTTGTTTTCAITTTAATAATCTCC
 39222 CTCCTCTTTACATTTTAAGCCAAGAAAGTATTCACTACTTTACTATATTAGCTGACCCTAATTTTGTCTTCTATCTATACTATCTATCC
 39313 TTATTTTCCAGTTTATTTTCCAAAGTTCTCTCTCTACAATTTTATTTATTTTAAATATTGTTTTAACTGTCTTCTCTATCTTGTCTTC
 39404 CTTTTCAAGATTTCAGAAAATGCTAATATACTCTCATTTTCTCAAACCTCAACAAAATGAATTAGAATCTACTAACTCTTTGAGGGCAT
 39495 ACATTTAGCATCTGGCTAGAGGAGGACCTCTGATGAAATTTAAATATACTAAAACTGCCCTTCTCAGGATGCTGTTAGTCCCTGCTACCAA
 39586 CTCTCTCTGTTTCTTTCTTTCTGTTTGTGTTTGTGTTTGTGTTTGTGAGGACAGCTCTGCTTGTCAACCAGGCTGGAGTGCAGT
 39677 GATGCAGCCTTGGCTCACTACAGCCTTGACCTCCTGGGCTCAGCCTCCACCTCAACCAGGCAAGTAGCTGAGGCTACAGGAGCATGCTAC
 39768 CACACCTGGCTGATTTTAAATTTTGTGAGAGATGGGCTCTCCCTATGTTGTCTAGGATGATCTGAATCTCTGGGTTCAAGTGATCCTC
 39859 CTGCTCAGCCTCCCAAAGTGTGGGATTACAGGATGAGGCACTGCACTCAGCCAGTATTTTCTTCCCCGAAAGCTCTTCTCTCTTAC
 39950 TTATCGCCATACAGGACTACTTAGCGAGGCTGTAGTTCAAGTTTGAAGGCTACCACTGTCCCAAAGTGTCTAGATACCCCTCTTGGCCT
 40041 GTGAAATACCTGTGATACAACAATAAATCACTCTCCAGCAGATGTTTGGACAATGACCTCTGGTGTCTCTTAAAGTTTCCAGTGGATT
 40132 AAATTTCTCTGATGCTCTTCTCTCTTTTCCAAGGGAGGCTTATATGAGACAGTTAATGAGGCTCTACAAGCTGGTCATCCCCATCCTAGAA
 40223 GCGCATCGAGAAATCCGGAAGCTGACACTCACTACAGCAAGCTGCAGAGAGCCTTCGACAGCATCGTTAAACAGGTAGCCGGGAGGCTG
 40314 GCTGGCAGGCTCTGTTACCTGGTGGCAGGCGACCTGTCTACAGATGCTTAGCCATCTTCTCTCCAGGGAGTGATTATCTTTAGCAC
 40405 ATTGCTTTTGTCTCACCTGTCAAACAGAAAAGGCTGAAATTTCTCTAACAGAGGACCAAAATTCATATGTGAAAACATACAGCTTAAA
 40496 TTACTTTATAACCAGGAAATGTGAGAAATTTTAAAGTGAATTTAAAGAAAGTCCAGAAATCTTTTATGGGATTCCTTTTGTGTTAATTC

$$\begin{array}{l}
 \text{1. } \frac{1}{2} \times \frac{1}{2} = \frac{1}{4} \\
 \text{2. } \frac{1}{2} \times \frac{1}{2} = \frac{1}{4} \\
 \text{3. } \frac{1}{2} \times \frac{1}{2} = \frac{1}{4} \\
 \text{4. } \frac{1}{2} \times \frac{1}{2} = \frac{1}{4} \\
 \text{5. } \frac{1}{2} \times \frac{1}{2} = \frac{1}{4} \\
 \text{6. } \frac{1}{2} \times \frac{1}{2} = \frac{1}{4} \\
 \text{7. } \frac{1}{2} \times \frac{1}{2} = \frac{1}{4} \\
 \text{8. } \frac{1}{2} \times \frac{1}{2} = \frac{1}{4} \\
 \text{9. } \frac{1}{2} \times \frac{1}{2} = \frac{1}{4} \\
 \text{10. } \frac{1}{2} \times \frac{1}{2} = \frac{1}{4}
 \end{array}$$

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50142 GATTATGCCACTGCGCTCCAGCCTGAGTGACAGAGTAAGACTCTGTCTCAAAAAACAACAATAAAAAAGAAAAATAATTTGGGCTGTGTATG
50233 GTGGCGACGCGCTGTAATCCACGCAATTGGGAGGCTGAGGTGGTGGATCCCTTGAGGCAGGAGTTCAAGACCAGCCTGGGCAATGTGGC
50324 AAAATCCCATCACTACAAAAAATACAAAAATAGCCAGGTATAGTGGCACACACCTGTAGTCTCAGCTACTTGGGAGGCTGACATGGGAGG
50415 ATCACTTGAGCCTGGGAAGTGGAGGCTGCACTGAGCAGAGATCATGCCACTGCTCTCTAGCCTGGGTGATAGAGCGAGACCCTGTCTAAAA
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50870 TTTTTTTTTTTTTTCCACAGGCGACCTGGAAGTAGCCCAAGTGTTTTGGCTGAAATTCCTGCTGATCCAAAACCTCTATCGACATCAC
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51234 TACTTGAATCTAATAGTAACAAACGCTCAACTATGAAACGCTTTTGTGGCTAGCATCCGCTGTGCCCTCAATCACTTGTGTAAAA
51325 CAAGTATCATCATCTTCTCATTTTACAAAAGAGGAATCAGAGGTTTCAGAGAGGAGATAATTTACTTAAGGTCACACAGACAGTTGGC
51416 AGCAGAGATGAGCTCAAACGAGTCTTCTGAATCCAAATAGTCCACATGTCCATCAATGTGCTGATATTCACCTGATGCAGTACAGTCCCA
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Discussion

59151 GAAGGTGTTAGCTAGCTGCTACTTCTGCAACAAAGACTAAGGAGAGTTTAGCTGATTTTACCAAGTTGTCCGAGTAGACTTCCCA
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Putative promoter sequence of human CLASP-5

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hCLASP5 -----MTHLNSLDVQLAQELG----- 16
hCLASP3 -----MAERRAFAQKISRTVAAEVRKQISGQYSGSPQLLNINIVG 41
hCLASP2 -----MLLFFPYDDFQTAILRRQGRYICS----- 23
hCLASP7 -----MAASERRAFAHKINRTVAAEVRKQVSRERSGSPHSSRRCSSSL 43
hCLASP1 MSFRGKVFKEPSEFWKKRRTVRRVIQEEFHRFSSQEKPRLLLEPLDYETVIEELEKTYRN 60
      ...

hCLASP4 -----STVPEDA EKRAQSLFVKECIKTYSTDWHVVNYK 53
hCLASP5 -----DFT 19
hCLASP3 N-----ISHHTTVPLTEAVDPVDLEDYLITHPLAVDSGPLRDLIEFP 83
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hCLASP7 G-----VPLTEVVEPLDFEDVLLSRPPDAEPGPLRDLVEFP 79
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      ::

hCLASP4 YEDFSGDFRMLPCKSLRPEKIPNHVFEIDEDCEKDED-----SSSLCSQKGGVIKQG 105
hCLASP5 DDDL DVVFTPKECRTLQP-SLPEEGVELDPHVR-----DCVQTYIREWLI 63
hCLASP3 PDDIEVVYSPRDCRTLVS-AVPEE-SEMDPHVR-----DCIRSYTEDWAI 126
hCLASP2 YEDYSGEFROLFNKVVKLDKLPVHVYEVDEVDKDED-----AASLGSQKGGITKHG 107
hCLASP7 ADLELLQLPRECRTEP-GIPKD-EKLDQVR-----AAVEMYIEDWVI 122
hCLASP1 YEQYSGDIRQLPRAEYKPEKLPSSHSEIDHEDADKDEDTTSHSSSKGGGGAGGTGVFKSG 180
      :: .      : * . : * .

hCLASP4 WLHKANVNSTIT--VTMKVFKRRYFYLTQLPDGSYILNSYKDEKNSKESK-GCIYLDACI 162
hCLASP5 VNRKNQGSPEIC--GFKKTGSRKDFHKT-LPKQTFESETLECSEPAQA--GPRHLNVLC 118
hCLASP3 VIRKYHKLGTGF--NPNTLDKQKERQKG-LPKQVFESDEAPDGNYSQDDQDDLKRRSMSI 183
hCLASP2 WLYKGNMNSAIS--VTMRSFKRRFFHLIQLGDGSYNLNFYKDEKISKEPK-GSIFLDSCM 164
hCLASP7 VHRRYQYLSAAY--SPVTTDTQRE RQKG-LPRQVFEQDASGDERSGPEDSNDSSRRGSGSP 179
hCLASP1 WLYKGNFNSTVNNTVTVRSEFKKRYFQLTQLPDNSYIMNFYKDEKISKEPK-GCIFLDSCT 239
      : :      : : * : : : :

hCLASP4 DVVQCPKMRRAHAFELKMLDKYSHYLA AE TEQEME EWLITLKKIIQINTDSL VQEKKETVE 222
hCLASP5 DVSGKGPVTACDFDLRSLQPDKRLENLLQQVSAEDFEKQNEEARRTN-----RQAE 169
hCLASP3 DDTPRGSWACSI FDLKNSLPDALLPNLLDRTPNEEIDRONDDQRKSN-----RHKE 234
hCLASP2 GVVQNNKVRRAFELKMQDKSSSYLLAADSEVEME EWITILNKILQLN-----FEAAMQEK 219
hCLASP7 EDTPRSSGASSI FDLRNLAADSLPSLLERAAPEDVDRRNETLRQH-----RPPA 230
hCLASP1 GVVQNNRLRKYAFELKMNLDLTYFVLA AE TESDMDEWIHTLNRILQISPEGPLQGRSTEL 299
      * : :      : : : :

hCLASP4 TAQDDETSS----QGKAENIMASLERSMHP ELMKYGRETEQLNKL SRGDGRQNLFSDSE 278
hCLASP5 LFALYPSVD----EEDAVEIRPVPEC PK EHLG-----N-----RILVKLLTLKFEIE 212
hCLASP3 LFALHPSPD----EEPIERLSVPDIPKEHFG-----QRLLVKCLSLKFEIE 277
hCLASP2 RNGDSHEDD----EQSKLEGSGSGLDSYLP ELAKSAREAEIK---LKSES RVKLFYLDPD 272
hCLASP7 LLTLYPAPD----EDEAVERCSRPEPPREHFG-----QRI LVKCLSLKFEIE 273
hCLASP1 TDLGLDLSLNSVTCECTPEETDS ENNLHADFAKYLTETEDTVKTTNRMERLNLFS LDPD 359
      :      : : : : :

hCLASP4 VORLDFS----GIEPDIKP-FEEKCNKRFLVNCHDLTFN I LGQIGNAKGPPTNVEPFFI 333
hCLASP5 IEPLFAS----IALYDVKERKKI SENFHC DLNSDQFKGFLRAHTPSVAASSQARS AVFSV 268
hCLASP3 IEPIFAS----LALYDVKEKKI SENFYFDLNSEQMKGLLRPHVPPAAITTLARSAIFSI 333
hCLASP2 AQKLDFS----SAEPEVKS-FEEKFGKRILVKCNDLSFNLQCCVAENE EGPTTNVEPFFV 327
hCLASP7 IEPIEGL----LALYDVREKKI SENFYFDI NSDSMKGLIRAHGTHPAISTILARSAIFSV 329

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hCLASP4	NLALFDVKNCKISADFHVDLNPSPVREMLWGSSTQLASDGP---	KGSSPESYIHGIAE	390
hCLASP5	TYPSSDIYLVVKIEKVLQOQD----	IGDCAEPTYVIKESDG-----	GKSKE-KIEKLLK 317
hCLASP3	TYPQDVLFLVIKLEKVLQOQD----	IGECAEPMIFKEADA-----	TKNKE-KLEKLLK 382
hCLASP2	TLSLFDIKYNRKISADFHVDLNFHFSVRQMLATTSPALMNGS-----	GQSPSVLKGILHE	381
hCLASP7	TYPSPDI FLV I KLEKVLQOQD----	ISECCEPYMVLKEVDT-----	AKNKE-KLEKLRL 378
hCLASP1	SVALYDLDRSRKISADFHVDLNHAAVRQMLLGASVALENGNIDTITPRQSEEPHIKGLPE		479
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hCLASP4	SQLRYIQQGISVVTNPHPEIFLVARIEKVLQGNITHCAEPIKNSDPVKTAQKVHRTAKQ		450
hCLASP5	QAESFCQR-----	LGKYRMPFAWAPISLSSFFNVSTLEREVDVDSVVGRSPVGERRTLA	372
hCLASP3	QADQFCQR-----	LGKYRMPFAWTAIHLNIVSSAGSLERDSTEVEISTGERKGSWSERR	437
hCLASP2	AAMQYQKQGISVTPHPDIFLVARIEKVLQGSITHCAEPMKSSDSSKVAQKVLKNAKQ		441
hCLASP7	AAEQFCTR-----	LGRYRMPFAWTAVHLANIVSSAGQLDRDSD----	SEGERRPAWTD RR 429
hCLASP1	EWLKFQKQAVFSVSNPHSEIVLVAKIEKVLGMNINASGAEPYIKNPDSNKYAQKILKSNRQ		539
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hCLASP4	VCSRLGQYRMPFAWAARPIFKDTQGSLLDGRF	FSPLYKQDSSKLSSEDIKLLSEYKKPE	510
hCLASP5	QSRLSERALSLEENGVSFNKTS-----	TLVSSFFKQEGDRLSDEDLFKFLADYKRSS	427
hCLASP3	NSSIVGRSLERTTSGDDACNLTSFR-PATLT	VTNFFKQEGDRLSDEDLFKFLADMRPS	496
hCLASP2	ACQRLGQYRMPFAWAARTLFDASGNLDKNARFSAIYRQDSNKLSDNDMLKLLADFRKPE		501
hCLASP7	---RRGPQ---	DRASSGDDACSFSGFR-PATLT	VTNFFKQEAERLSDEDLFKFLADMRPS 483
hCLASP1	FCSKLGKYRRFAWAVRSVFKDNQGNVDRDSR	FSPLFRQESSKISTEDLVKLVSDYRRAD	599
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hCLASP4	--KTKLQIIPGQLNITVECVPVDSNLCITSSYVPLKPFE-KNCQNITVEVEEFVPEMTKY		567
hCLASP5	SLQRRVKSIPGLLRLEISTAPEIINCCLTPEMLPVKPPF-ENRTRPHKEILEFP--	TREV	484
hCLASP3	SVLRLRPITAOBKIDISPAPENPHYCLTPELLQVKLYP-DSRVRPTREILEFP--	ARDV	553
hCLASP2	K-MAKLPVILGNLDITIDNVSSDFPNYVNSSYIPTKQFETCSKTPITFEVEEFVPCIPKH		560
hCLASP7	SLLRLRPVTAOLKIDISPAPENPHFCLSPPELLHIKYP-DPRGRPTKEILEFP--	AREV	540
hCLASP1	R-ISKMQTIPGSLDIAVDNVPLEHPNCVTSSFI PVKPFNMMAQTEPTVEVEEFVYDSTKY		658
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hCLASP4	CYPFTIYKNHLYVYPLQLKYDSQKTFAKARNIAVCVEFRDSDSDASALKCIYKGPAGSV		627
hCLASP5	YVPHTVYRNLLYVYPQRLNFVN--	KLASARNITIKIQFMCQ-EDASNAMPVIFGKSSGPE	541
hCLASP3	YVPNTTYRNLLYIYPQSLNFAN--	RQGSARNITVKVQFMYG-EDPSNAMPVIFGKSSCSE	610
hCLASP2	TQPYTIYTNHLYVYPKLYKYDSQKSFAKARNIAICIEFKDSDEEDSQPLKCIYGRPGGPV		620
hCLASP7	YAPHTSYRNLLYVYPHSLNFSS--	RQGSVRNLAVRVQYMTG-EDPSQALPVIFGKSSCE	597
hCLASP1	CRPYRYVKNQIYIYPKHLKYDSQKCFNKARNITVCIEFKNSDEESAKPLKCIYKGPESPL		718
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hCLASP4	FTTNAYAVVSHHNQNPFEYDEIKIELPIHLHQKHLLFTFYHVSC	INTKGTTKKQDIVE	687
hCLASP5	FLQEVYTAVTYHNKSPDFYEEVKIKLPAKLTVNHLLFTFYHISCO	-----KOGASVE	595
hCLASP3	FSKEAYTAVVYHNRSDFHEEIKVKLPATLTDHHLLFTFYHVSC	-----KONTELE	664
hCLASP2	FTRSFAAVALHHRQNPFEYDEIKIELPTQLHEKHLLFTFYHVSC	-----KONTELE	680
hCLASP7	FTRFAFTPVVYHNKSPDFYEEFKLHLPACVTENHLLFTFYHVSC	-----RPGTALE	651
hCLASP1	FTSAAYTAVLHHSQNPDFSDEVKIELPTQLHEKHILFSFYHVTCDINAKANAKKKEALE		778
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hCLASP4	TPVGFAWVPLLKDGRIITFEQQLPVSA	NLPPGYLNLNDAESRRQCNVLIKWVDGAKPLLK	747
hCLASP5	TLLGYSWLPILLNERLQTSYCLPVALEKLP	PNYSMHSAEKVPLQNPFIKWAEGHKG VFN	655
hCLASP3	TPVGTYWIPMLQNGRLKTGQFCLPVSL	LEKPPQAYSVLSPEVP---LPGIKWVDNHHKG VFN	721
hCLASP2	TQVGYSWLPILLKDRVVTSEQHIVPSANLPSGHLGYQELGMGRHYGPEIKWVDGKPLLK		740
hCLASP7	TPVGFTWIPLLQHGRLRTGPFCLPVSDQPPPSYSVLTPDVA---	LPGIKWVDGHHKG VFN	708
hCLASP1	TPVGYSWLPILLKDRVVTSEQHIVPSANLPSGHLGYQELGMGRHYGPEIKWVDGKPLLK		838

Cadherin EC motif

hCLASP4	PMFAFAKPKLQR-----VQDS--NLEYSLSD EYCKHFLVGLLLRETSI	1060
hCLASP5	FFMNLDTAPTSP--CPSISSNSSSSCSSFVQDKIASFMLDTSYRQHFHFLTGILFTLEAA	1085
hCLASP3	CSLLTAPSPSPSVSSATSQSSGFSNVQDKIANMFELSVPPRQHYLAGIVLTELAV	1196
hCLASP2	PMPFKGKRIQR-----YQDL--QLDYSLTDFECRNHFVGLLLREVTG	1052
hCLASP7	PCCCLSPSPSPSPSVSSTTSQSSTFSSQAPDPKVTSMFELSGPFRQHFFLAGILLETAL	1119
hCLASP1	PIRSANIPDPLTP-----SES---TQELHASDMPEYSVTNEFCRKHFLIGILLREVG	1157

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hCLASP4      ALQDN----YEIRYTAISVIKNLLIKHAFDTRYQHKNQQAIAQLYLPFVGLLENIDRL 1116
hCLASP5      ALDAEGEIGISKVQRKAVSAIHSLLSSHDLDPRCVKPEVKVIAALYLPVIGIILDLP-- 1143
hCLASP3      ILDPAEGLFGLHKHNVINHVNLLSSHSDSPRYSDPQIKARVAMLYLPVIGIMETVP-- 1254
hCLASP2      ALQEFR-----EVRLIAISVLKNLLIKHSFDDRYASRSHQARIATLYLPVGLLIENVQRI 1108
hCLASP7      ALPEPAEGAFILHKKAISA VHSLLCGHDTDPRYAEATVKARVAELYLPVLLSIARDTLP-- 1177
hCLASP1      ALQEDQ----DVRHLALAVLKNLMKHSFDDRYREPRKQAIASLYMPVLYGMLLDNMPRI 1213

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hCLASP4	AGRDTLYSCA-----AMPN-S---ASRDEFPCGFTSPANRGSLSTDKDTAYGS	1160
hCLASP5	-----QL-----CDFTVADTRRYRTSGSD-	1162
hCLASP3	-----QLY-----DFTETHNQRGRPCIIATDD--	1276
hCLASP2	NVRDVSFFPVNAGMTVKDESIALPA-VNPLVTPQKGSTLDNSLHKDLLGAISGLIAPYTT	1167
hCLASP7	-----RLH-----DFAEGPGQRSLRLASMLSDSTE	1201
hCLASP1	YLKDLYPFTVNTSNQGSRDDLSTNGGFSQSQTAIKHANSVDTFSKDVLSIAAFSSIAIS	1273

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hCLASP4      FQ-NGHGIKREDSRGSLIPEGATGFDPQNGTGEN-----TRQSSSTRSSVSQYNRLDQYE 1213
hCLASP5      -----EEQEGAGAIINQVALAIAGNNFNFLT-----SGIVLSSLPYKQYNMLNADT 1208
hCLASP3      -----YESESGSMISQTVAMAIGTSVPQLTR-----PGSFLTSTSGRQHTTFSAES 1324
hCLASP2      STPNINSVRNADSRGSLISTDGSNSLPERNSEKSNLSLDKHQSSSTLGNSSVVRCKDLQDSE 1227
hCLASP7      -----GEGDIAGTINPSVAMAIAAGGPLAPGSR----ASISQGPPTASRAGCALSAES 1249
hCLASP1      -----TVNHADSRASLASLDSNPSTNEKSSEKTDNCEKIPRPLALIGSTLRFDRDLQAE 1327

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hCLASP4	IRSLLMCYLYIVKMISEDTLLTYWNKVSPQELINILILLEVCLFHFRYMGKRNIARVHDA	1273
hCLASP5	TRNLMICFLWIMKNADQSLRKWIADLPSTQLNRILDLLFCVLCFEYKGKQSSDKVSTQ	1268
hCLASP3	SRLLICLLVLNKNADETVLQKWIDLTVLQLNRRLLDLLYLVCSCFEYKGKKVFERNMSL	1384
hCLASP2	IKSLMLMCFYILKSMDDALFTYWNKASTSELMDFFTISEVCLHQFYMGKYIARNQEG	1287
hCLASP7	SRTLACVLVWLKNTPEALLQRWATDLTLPQLGRLLDLLYLCLAAFEYKGKKAFFERINSL	1309
hCLASP1	IRSLLMCFLHMKTISYETLIAYWQRAPSPVEVSDFISILDVCLQNFRYLGLKRNIIIRKIAA	1387

hCLASP4	WLSKHFGIDR-----	KSQTMPALNRNSGVMAQLRLQHLSSLESS-----	1311
hCLASP5	VLQKSRDVKAR-----	LEEALLRGEGARQEMRRRAPGNDRSPGLNEN-----	1311
hCLASP3	TFKKSKDMRAK-----	LEEALIGSIGARQEMVRRSRQGRSPGSAGFSQ-----	1430
hCLASP2	LGPVIVHDKRS-----	QTLFVSRNRTGMHARLQQLGSLDNS-----	1323
hCLASP7	TFKKSLDMKAR-----	LEEALIGTIGARQEMVRRSRERSPFGNPEN-----	1350
hCLASP1	AFKFVOSTQNNGTLGKSNPSCQTSGLLAQWMHSTSRHEGHQKQRSQTLPIIRGKN-----	1442	

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hCLASP4      -----FTLNHSSSTTETDIFHQALLEGNTATEVSLTVLDTISFFTCQFKTQLL 1359
hCLASP5      ---LRWKKEQTHWRQANEKLDKTKAELDQEAALISGNLATEANLIILDMQENITQASS-ALD 1368
hCLASP3      ENLRWRKDMTHWRQNTKELDKSRAEIEHEALIDGNLATEANLIILDTLEIVQTVS-VTE 1369
hCLASP2      -----LTFNHSYGHSDADVLHQSLLEANIATEVCLTALDTLSLFTLAFKNQLL 1371
hCLASP7      ---VRWRKSVTHWKKQTSRDVDTKDEMEHEALVEGNLATEASLVLVDLTLEIIVQTM-LSE 1407
hCLASP1      --AISNPKLLQMLDNTMTSNESEIDVHHVDTEANIATEGCLTLDLVSLFTOTHOROLO 1500

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hCLASP4 NNDGHNPLMKKVFVDIHLAFLKNGQSEVSLKHVFASLRAFISKFPSAFFKGRVNMCAAFY 1419
hCLASP5 CKDS---LLGGVLRVLVNSLNCDDQSTTYLTHCFATLRALIAKFGDLLFEEVEQCDFDLCH 1425
hCLASP3 SKES---ILGGVLRVLLHSMACNQSAVYLQHCFTQALVSKFPELLFEEETEQCADLCL 1546
hCLASP2 ADHGHNPMLKKVFDVYLCLFQKHQSETALKNVFTALRSIYKFPSTFYEGRADMCALCY 1431
hCLASP7 ARES---VLGAVLKVVLYSLGSAQSALFLQHGLATQALVSKFPELLFEEDTELCAIDLCL 1464
hCLASP1 QCDCQNSLMKRGFDTYMLFFQVQNQSATALKHVFASLRLFVCKFPSAFFQGPADLCGSFCY 1560
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hCLASP4 EVLKCCTSKISSTRNEASALLYLLMRNNFEYTKRKTFLRTHLQIIIAVSQLIADVALSGG 1479
hCLASP5 QVLHHCSSSMDVTRSQACATLYLLMR--FSFGATSNFARVKMQVTMSLASLVGRAPDFNE 1483
hCLASP3 RLLRHCCSSSIGTIRSHPSASLYLLMR--QNFEIGNNFARVKMQVPMSLSSLVGTSONFNE 1604
hCLASP2 EILKCCNSKLSSIRTEASQLYFLMRNNFDYTGKKSFVRTHLQVIIISVSLIADVVGIGE 1491
hCLASP7 RLLRHCGSRISTIRTHASASLYLLMR--QNFEIGNNFARVKMQVTMSLSSLVGTTONFSE 1522
hCLASP1 EVLKCCNHRSRSTQTEASALLYLFMRKNFEFNKQKSIVRSHLQLIKAVSOLIADAG-IGG 1619
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hCLASP4 SRFQESLFIINNfansDRPMKATAFFAEVKDLTKRIRTVLMATAQMKHEKDPPEMLIDLQ 1539
hCLASP5 EHLRRLSLRTILAYSEEDTAMQMPFPTQVEELLCLNLSILYDVKMREFOEDPEMLMDLM 1543
hCLASP3 EFLRRLSKTILTYAEEDLELRETTFPDQVQDLVFNLMILSDTVKMKHEQEDPEMLIDLQ 1664
hCLASP2 TRFQQSLSIINNCLNSDRLLKHTSFSSDVKDOLTKRIRTVLMATAQMKHEHNDPEMLVDLQ 1551
hCLASP7 EHLRRLSKTILTYAEEDMGLRDS TFAEQVQDLMFNLHMILTDTVKMKHEQEDPEMLIDLQ 1582
hCLASP1 SRFQHSLATINNfANGDKQMKNSNFAEVDLTKRIRTVLMATAQMKHEKDPPEMLVDLQ 1679
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transmembrane
hCLASP4 YSLAKSYASTPELRKTWLDMAKIHVKNGDIFSEAMCYVHVAALVAEFLHRKK----- 1592
hCLASP5 YRIAKSYQASPDRLRLTWLQNMAGEKHTKKKQYTEAMCLVHAAALVAEYLSMLEDH----- 1598
hCLASP3 YRIAKGYQTSFE-RLTWLQNMAGKHSERSNHAEEAQCCLVHSAALVAEYLSMLEDR----- 1718
hCLASP2 YSLAKSYASTPELRKTWLDMAKIHVKNGDILSEAMCYVHVTALVAEYLSMLEDR----- 1604
hCLASP7 YRIARGYQGSFDRRLTWLQNMAGKHAELGNHAEEAQCCLVHAAALVAEYLSMLEDR----- 1637
hCLASP1 YSLANSYASTPELRRTWLESMAKIHARNGDILSEAMCYIHIAALIAEYLSMRKGYWKVEKI 1739
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hCLASP4 -----LFPNGCSAFKKITPNIDEEGAMKEDAGMMD----- 1622
hCLASP5 -----SYLPVGSVSFQNISSNVLEESVVSSEDTLSPDEEDGV 1633
hCLASP3 -----KYLPGCVTFQNISSNVLEESAVSDDVSPDEEGI 1753
hCLASP2 -----VFRQGCTAFRVITPNIDEEASMMEDVGMQD----- 1634
hCLASP7 -----RHLPVGCVSFQNISSNVLEESAISDDILSPDEEGF 1672
hCLASP1 CTASLLSEDTHPCDSNSLLTTPSGGSMFSGWPAFLSITPNIKEEGAAKEDSGMHD----- 1795
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ITAM
hCLASP4 ---VHYSEEVILLELEQCVDGLWKAERYEIISEISKLVPIYEKRRREFEKLTVYRTIHG 1679
hCLASP5 CAGQYFTESGLVGLLEQAALFSTGGLYETVNEVYKLVIPILEAHREFRKLTLTHSKIQR 1693
hCLASP3 CSGKYFTESGLVGLLEQAASFSMAGMYEAVNEVYKLVIPILEANRDAKLLSTIHGKIQE 1813
hCLASP2 ---VHFNEVDLMELLEQCADGLWKAERYELIADIYKLIPIYEKRR----- 1677
hCLASP7 CSGKHFTENGLVGLLEQAAGYFTMGGLYEAVNEVYKLVIPILEAHRDYKKLAHVHGKIQE 1732
hCLASP1 ---TPYNENILVEQLYMCGEFLWKSERYELIADVNKPIIAVFEKQDRFKKLSLDLYDIHR 1852
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ITAM DOCK motif DOCK motif ITAM
hCLASP4 AYTKILEVMHTKRLGLTFFRVAFYGQSFFEEEDGKEYTYKEKRLTGLSEISLRVLKLYG 1739
hCLASP5 AFDSIVNKDH--KRMFGTYFRVGFYFG-SKFGDLLEQEFVYKEFAITKLPEISHRLEAFY 1750
hCLASP3 AFSKIIVHQSTGWERMFGTYFRVGFYFG-TKFGDLLEQEFVYKEFAITKLAEISHRLEAFY 1872
hCLASP2 -----IFFEDEDGKEYTYKEKRLTGLSEISQRLLKLYS 1710
hCLASP7 AFTKIMHQSSGWERVFGTYFRVGFYFG-AHFGDLLEQEFVYKEFSITKLAEISHRLEAFY 1791
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	ITAM	ITAM	
hCLASP4	ERFGTENVKIIQSDSKVNAKELDPHYAHIQV	TYVVKHYFDDKELTERKTEFERNHNISR	FV 1799
hCLASP5	QQFGAEFVEVIKIDSTPVDKTKLDPNKAYIQI	TFVEHYFDEYEMKDRVTYFEKNFNLRR	FM 1810
hCLASP3	ERFGEDVVEVIKDSNPVDKCKLDPNKAYIQI	TYVEHYFDTYEMKDRITYFDKNYNLRR	FM 1932
hCLASP2	DKFGSENVKMIQDSGKVNPKDLDSYAYIQV	THVIEFFDEKELQERKTEFERSHNIR	FM 1770
hCLASP7	ERFGDDVVEIIKDSYPVDKSKLDSKAYIQI	TYVEHYFDTYELKDRVTYFDRNYGLRT	FL 1851
hCLASP1	DKFGADNVKIIQDSNVKNPKDLDPHYAYIQV	TYVTFEEKEIEDRKTD FEMHHNINR	FV 1972

	ITAM	DOCK motif	
hCLASP4	FEAPYTLSGKKQGCIEEQCKRRTILTTSNSF	YVVKRIPINCEQQINLKPIDGATDEIK	D 1859
hCLASP5	YTFPFTLEGRPRGELHEQYRRNTVLTTMHAF	YIKTRISVIQKEEFVLTPIEVAIEDMK	K 1870
hCLASP3	YCTPFTLDGRAHGEHQFQRKTLTTSHAFF	YIKTRVNVTHKEEILTPIEVAIEDMQ	K 1992
hCLASP2	FEMPFTQTGKROGGVEEQCKRRTILTAHCF	YVVKRIPVMYQHHTDLNPIEVAIDEM	SK 1830
hCLASP7	FCTPFTPDGRAHGEHQHQRKTLTSDHAF	YIKTRIRVCHREETVLTPEVAIEDMQ	K 1911
hCLASP1	FETPFTLSGKKHGVAEQCKRRTILTSHLFF	YVVKRIRIQVISQSSTLNPIEVAIDEM	SR 2032

	Coiled-coil	
hCLASP4	KTAEQLKLCSSSTDVMIQLQLKLQGVWSV	QVNAVAGPLAYARAFND SQASKYPPKKVSELK 1919
hCLASP5	KTLQLAVAINQEPDPAKMLQMVLOGSVG	ATVNVQGPLEVAQVFLAEIPADPKLYRHHNKL 1930
hCLASP3	KTQELAFATHQDPADPKMLQMVLOGSVG	TVNVQGPLEVAQVFLSEIPSDPKLFRHHNKL 2052
hCLASP2	KVAELRQLC SSAEVDMIKLQLKLQGSV	SVQVNAVAGPLAYARAFDDTNTKRYPDNKVKLLK 1890
hCLASP7	KTRELAFAEQDPPDAKMLQMVLOGSVG	PTVNVQGPLEVAQVFLAEIPEDPKLFRHHNKL 1971
hCLASP1	KVSELNQLCTMEEVDMISLQLKLQGSV	SVKVNAGMAYARAFLEETNAKKYPDNQVKLLK 2092

	Coiled-coil	
hCLASP4	DMFRKFIQACS	ALELNERLIKEDQVEYHEGLKSNFRDMVKELSDIIEHQILQEDTMHSP 1979
hCLASP5	LCFKEFIMRCGE	AVEKNKRLITADQREYQELKKNYNKLKENLRPMIERKIPELYKPIFR 1990
hCLASP3	LCFKDFTKRCE	DALRKNKSLIGPVQKEYQRELGLSSP----- 2090
hCLASP2	EVFRQFVEACG	QALAVNERLIKEDQLEYQEEMKANYREMAKELSEIMHEQICPLEEKT- 1949
hCLASP7	LCFKDFCKKCE	DALRKNKALIGPDQKEYHRELERNYCRLREALQPLLTQRLPQLMAPTP- 2030
hCLASP1	EIFRQFADACG	QALDVNERLIKEDQLEYQEELRSHYKDMSELSTVMNEQITGRDDL SKR 2152

	PDZ ligand	
hCLASP4	WMSNTLHVFC	AISGTSSDRGYGSPHYAEV-- 2008
hCLASP5	VESQKRDS	FHRSSFRCETQLSQS----- 2015
hCLASP3	-----	-----
hCLASP2	VLPNSLHIF	NAISGTPSTMVHGMTSSSSVV 1980
hCLASP7	--PGLRNSL	NRASFRKADL----- 2047
hCLASP1	GVDQTC	TRVISKATPALPTVSISSSAEV-- 2180